



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 102238

TO: Minh-Tam Davis  
Location: CM-1/8A01/8E12  
Art Unit: 1642  
Thursday, August 28, 2003

Case Serial Number: 09/554945

From: Mary Jane Ruhl  
Location: Biotech-Chem Library  
CM1-6A06  
Phone: 605-1155

maryjane.ruhl@uspto.gov

### Search Notes

Examiner Davis,

Here are the results for your recent search request.

*sgt/28*

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl  
Technical Information Specialist  
STIC  
CM-1, Rm. 6-A-06  
605-1155

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960 CCGAGATCAGATGGGAAATACACAGAAAGTACTCCGGTGGCAGCAGTCCAAGATG 1019  
 QY 1001 GTCTTGCTAAGGAGAAACAGATGAACACAGTATCTAACACATTAACCTTGACAAATGGCT 1060  
 Db 1020 GCTTCACTAACCGTGAAACAGTACAGAGCGTGTCTAACACACCTTGACCTTGCCAATGGCT 1079  
 QY 1061 TGGAAAGGAGAACTAAACCTTACAGTGAAGCACTTTAGGACTTCCATATTTCCCA 1120  
 Db 1080 TGGAAAGGAGAACTAAACCTTACAGTGAAGCACTTTAGGACTTCCATATTTCCCA 1139  
 QY 1121 ATTTCTATCGCTACTGAAAGTATTTGATTCAGAAAAAGAGCAAAAGAGAGAAAGAAC 1180  
 Db 1140 ACTTCTATGCACTACTGACAGCATCGACTCAGAAAAAGAGCAAAAGAGAGAAAGAAC 1199  
 QY 1181 TGATTACTATGATGAACACACTGATGATGATTTGGAAGATGATGATGATGATGATGATG 1240  
 Db 1200 TGATCACCATCATGAAGACATGATGATGATTTGCTGCTGCTGCTGCTGCTGCTGCTG 1259  
 QY 1241 TATCTCCAGAGAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1300  
 Db 1260 TATCTCCAGAGAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1319  
 QY 1301 CCAAAACAAAGTACAAAAAATGCTACTGACATATATGAAGCAAGCTTTTCCAGCAGCAT 1360  
 Db 1320 CCAAGAACAGCTAGAAAAAATACTACTGATGACAAAGTAAAGCTATTTCCAGCTCCAC 1379  
 QY 1361 CAGAGAGAGTCTAGAAACACAGACATACCAAGGAAGAGAGCAGCTAAGATGGAAGAG 1420  
 Db 1380 CAGAGAGAGTCTAGAAACACAGACATACCAAGGAAGAGAGCAGCTAAGATGGAAGAG 1439  
 QY 1421 ATATGGAAGCTTGAAGATTCACAAAGATGATTAACCTCAACCCAGGAGAGAGAGAG 1480  
 Db 1440 ATATGGAAGCTTGAAGATTCACAAAGATGATTAACCTCAACCCAGGAGAGAGAGAG 1499  
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 Db 1500 ATGAACCCAAAGGAG 1559  
 QY 1541 TGAAGAACATGACAAAG 1600  
 Db 1560 TGAAGAACATGACAAAG 1619  
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 QY 1721 ACTGTTTCAGAAACATATATAGCTTAAACACATTTCTAAATTTCTGATTAATAATTTT 1780  
 Db 1738 GTTGTTCAGCAAAACATATAGCTTAAACACATTTCTAAATTTCTGATTAATAATTTT 1793  
 QY 1781 GACCCAGAGGTTATAGAGAGTCTGAAATTTTACAGTACTTAACTTTTACAGTCTGTTAA 1840  
 Db 1794 CAGCCAGAGGTTATAGAGAGTCTGAAATTTTACAGTACTTAACTTTTACAGTCTGTTAA 1853  
 QY 1841 ACATAGCTTTCTCCCGTAAAAATATCTG-AAAAGTAAAGTGTATGATTAAGCTGAGATT 1899  
 Db 1854 ATAGAGCTCTCTGCGCATTAATACCTTATGAAAGCAAGAGCTGTAGAGAACCCGAGGTT 1913  
 QY 1900 TTGTATACAGGATCCTTTATTTCTCATAGNCTTATTTATTTATATACAGGAAATATGTTG 1959  
 Db 1914 TTCTATATAGAACTCTTTATTTCTCATAGNCTTATTTATTTATATACAGGAAATATGTTG 1972  
 QY 1960 CTTTGGAAAA 1969  
 Db 1973 CTCTGGAAAA 1982

RESULT 9  
 RNSGIII

RNSGIII 2146 bp mRNA linear ROD 07-DEC-1994  
 Rattus norvegicus secretogranin III (SgIII) mRNA, complete cds.  
 U02983  
 U02983.1 GI:413765  
 Rattus norvegicus (Norway rat)  
 ORGANISM  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 2146)  
 Dopazo, A., Lovenberg, T.W., Danielson, P.E., Ottiger, H.P. and  
 Sutcliffe, J.G.  
 Primary structure of mouse secretogranin III and its absence from  
 deficient mice  
 J. Mol. Neurosci. 4 (4), 225-233 (1993)  
 95001263  
 PUBMED 7917832  
 2 (bases 1 to 2146)  
 Dopazo, A.  
 Direct Submission  
 Submitted (28-OCT-1993) Dopazo A., The Scripps Research Institute,  
 Molecular Biology, 10666 N. Torrey Pines Rd., La Jolla, CA 92037,  
 USA  
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 Location/Qualifiers  
 1..2146  
 /organism="Rattus norvegicus"  
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 /db\_xref="taxon:10116"  
 296..1711  
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 /codon\_start=1  
 /product="secretogranin III"  
 /protein\_id="AAA56637.1"  
 /db\_xref="GI:413766"  
 691 a 523 c 496 g 436 t  
 ORIGIN  
 Query Match 60.6%; Score 1221.6; DB 10; Length 2146;  
 Best Local Similarity 79.4%; Pred. No. 2.2e-250;  
 Matches 1584; Conservative 0; Mismatches 370; Indels 41; Gaps 10;  
 QY 1 TAAAGCTACGCCCTTACCTGAGACTTGCCTCCGCGCCGCCCAACCTGCTTATCCCT 118  
 Db 9 TAAAGCTACGCCCGCCGCGCTCGCAGCGCGCGAGCGAGAACTTCAGCAGCCGCGGGCG 68  
 QY 59 GACAGCGCTCCCTTACCTGAGACTTGCCTCCGCGCGCCGCCCAACCTGCTTATCCCT 128  
 Db 69 GACAGCGCGCCGCGCACCTGCTGCTCCGCGCGCGCGAGAGCGACATCCTCTCTG 128  
 QY 119 TGACCGCTGAGTGTGAGAGATCTTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 178  
 Db 129 CCAGCGCGCTGAGAGTGCACCGGGGGCGG-----CCAGAGTCTCTCTCTCTCTG 181  
 QY 179 CCCACCTCCCGGCTCTTCTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 238  
 Db 182 CCCAGGCTCTGCT 241  
 QY 239 CTCAGAGCGCCGCGCGGGGCTGT-----GACCAAGCGCGAGCTGGAAGATGGG 290  
 Db 242 CT-CAGGGCGCGCGCGCAAGCTCTTCCAGCAGAGCGAGAGAGAGAGAGAGAGAGAG 300  
 QY 291 GTTCTCTCGGAGCGGCACTTGGATTCTGTGTAGTCT-----CCGATTCAAGC 341

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2003, 08:23:38 ; Search time 70 Seconds  
(without alignments)  
1061.201 Million cell updates/sec

Title: US-09-554-945B-2

Perfect score: 2402

Sequence: 1 MGFLGTGTWILVLPQAF.....EKGILDKKEAEAIRKRYSSL 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2402	100.0	468	21 AAY81955	Human HsgIII prote
2	2384	99.3	468	21 AAB18926	A novel polypeptid
3	2384	99.3	468	22 AAB12216	Human PRO5990 poly
4	2384	99.3	468	22 AAB87600	Human PRO5990, Ho
5	2384	99.3	468	23 ABG95925	Human secreted/tra
6	2384	99.3	468	24 ABU69097	Human PRO polypept
7	2384	99.3	468	24 ABU69120	Human PRO polypept
8	2384	99.3	468	24 ABU71580	Human secreted pol
9	2384	99.3	468	24 ABU72026	Novel human secret

10	2384	99.3	468	24 ABU72183	Human PRO polypept
11	2384	99.3	468	24 ABU66614	Human PRO polypept
12	2384	99.3	468	24 ABU66890	Human secreted/tra
13	2384	99.3	468	24 ABU59695	Novel secreted and
14	2384	99.3	468	24 ABG73287	Human neurosecret
15	2384	99.3	567	22 AAO13905	Human polypeptide
16	2384	99.0	468	22 AAM93910	Human polypeptide
17	2289	95.3	470	22 ABG12976	Novel human diagno
18	2093.5	87.2	471	23 ABB57046	Mouse ischaemic co
19	1989	82.8	396	24 AAO16322	Human secreted pro
20	597	24.9	316	22 ABG14006	Novel human diagno
21	472	19.7	212	22 ABG14003	Novel human diagno
22	182	7.6	665	21 AAB18278	Plasmodium falcipa
23	173.5	7.2	1881	23 ABP73809	Candida albicans e
24	173	7.2	1099	19 AAW40538	Mutant C-beta prot
25	173	7.2	1558	21 AAB18324	Plasmodium falcipa
26	173	7.2	1786	18 AAW24790	P. falciparum live
27	173	7.2	1787	23 AAU96699	Plasmodium falcipa
28	172.5	7.2	1979	21 AAB18171	Plasmodium falcipa
29	172	7.2	493	13 AAB26944	P.falciparum ISA g
30	172	7.2	1164	19 AAW40537	Group B streptococ
31	171	7.1	1093	19 AAW40540	Mutant C-beta prot
32	169.5	7.1	1164	17 AAR83781	Group B Streptococ
33	169.5	7.1	1164	21 AAY84459	Amino acid sequenc
34	169.5	7.1	1392	20 AAY06999	Restin protein seq
35	169	7.0	1129	21 AAY84462	Amino acid sequenc
36	168	7.0	1164	19 AAW40541	Mutant C-beta prot
37	168	7.0	1164	21 AAY84463	Amino acid sequenc
38	168	7.0	1254	11 AAR07503	Merozoite apical-en
39	168	7.0	1254	18 AAW24575	Merozoite apical-e
40	167	7.0	1427	12 AAR10534	Human 160kD mediat
41	166	6.9	1128	19 AAW40539	Mutant C-beta prot
42	166	6.9	1128	21 AAY84461	Amino acid sequenc
43	165.5	6.9	1788	22 ABG62995	Drosophila melanog
44	165	6.9	1135	21 AAY84460	Amino acid sequenc
45	163	6.8	309	22 ABG12975	Novel human diagno

## ALIGNMENTS

RESULT 1  
AAY81955  
ID AAY81955 standard; Protein; 468 AA.

XX AAY81955;

AC AAY81955;

XX 07-JUL-2000 (first entry)

DT Human HsgIII protein.

DE Human; secretogranin; HsgIII; NPCABC08 protein; SgIII family; cancer;

KW leukaemia; diabetes mellitus; kidney disease; autoimmune disease;

KW diagnosis; therapy.

XX Homo sapiens.

XX WO200017349-A1.

XX 30-MAR-2000.

XX 22-SEP-1998; 98WO-CN00199.

XX 22-SEP-1998; 98WO-CN00199.

XX (UYSH-) UNIV SHANGHAI SECOND MEDICAL.

XX Chen J, Fu G, Song H;

XX WPI; 2000-283577/24.

XX N-PSDB; AAA07414.

XX New NPCABC08 polypeptide comprising a 468 amino acid sequence, useful



XX WPI: 2000-628263/60.  
DR N-PSDB; AAA96353.  
XX  
PT Novel secreted and transmembrane polypeptides useful for diagnosing  
PT tumour in a mammal, for identifying agonists and antagonists of the  
PT polypeptide and for therapeutic use  
XX  
PS Claim 12; Fig 36; 222pp; English.  
XX  
CC The present sequence represents a secreted or transmembrane polypeptide.  
CC The specification describes polypeptides designated PRO1484, PRO4334,  
CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,  
CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO5990, PRO5990,  
CC PRO6030, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is  
CC useful for diagnosing tumour in a mammal. The polypeptides, their  
CC agonists and antagonists are useful treating a condition associated with  
CC expression or activity of the polypeptide. Conditions treated include  
CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are  
CC capable of inducing proliferation of mammalian kidney mesangial cells  
CC and are therefore useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Bergers disease or other  
CC nephropathies associated with Schonlein-Henoch purpura, celiac disease,  
CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used  
CC to generate transgenic animals for use in development and screening of  
CC therapeutically useful reagents and also for chromosome identification  
CC and tissue typing.  
XX  
SQ Sequence 468 AA;  
  
Query Match 99.3%; Score 2384; DB 21; Length 468;  
Best Local Similarity 99.1%; Pred. No. 2.3e-145;  
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 MGFLGTGWLVLVLPQIAFPKPGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP 60  
Db 1 MGFLGTGWLVLVLPQIAFPKPGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP 60  
  
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Db 61 ENKPGQSNYSFVDNLNLLRAITEKEKIEKQSISSPLDNKLNVEDVDSTKNRKLIDDY 120  
  
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Db 121 DSTKSGDLHKFODDPDGLHLDGTPLTAEDIVHKTAARIYEENDRAVFDKIVSKLLNLGL 180  
  
QY 181 ITESQAHTLEDEVAEVLKLSKEANNYEEDPNKPTSTENOAGKIPEKVTMPAAIQDGL 240  
Db 181 ITESQAHTLEDEVAEVLKLSKEANNYEEDPNKPTSTENOAGKIPEKVTMPAAIQDGL 240  
  
QY 241 AKGENDETVSNLTLTNGLERTKTYSNDFRDFQYFPNFYALLKSIDSEKAEKETLI 300  
Db 241 AKGENDETVSNLTLTNGLERTKTYSNDFRDFQYFPNFYALLKSIDSEKAEKETLI 300  
  
QY 301 TIMKTLIDFVMMVYGTISPEGVSYLENDEMIALQTKNKKLEKATNDSKLPAPSE 360  
Db 301 TIMKTLIDFVMMVYGTISPEGVSYLENDEMIALQTKNKKLEKATNDSKLPAPSE 360  
  
QY 361 KSHEETDSTKEAAKWEKYEGLSKDSTKDDNSPGCKTDEPKGTEAYLEAIRKNIEWLK 420  
Db 361 KSHEETDSTKEAAKWEKYEGLSKDSTKDDNSPGCKTDEPKGTEAYLEAIRKNIEWLK 420  
  
QY 421 KHKDKGNKEDYDLSKMRDFINKQADAYVEKGLDKAEAEATKRIYSSL 468  
Db 421 KHKDKGNKEDYDLSKMRDFINKQADAYVEKGLDKAEAEATKRIYSSL 468  
  
RESULT 3  
AAU12216  
ID AAU12216 standard; Protein; 468 AA.  
XX  
AC AAU12216;  
XX

DT 24-OCT-2001 (first entry)  
XX  
DE Human PRO5990 polypeptide sequence.  
XX  
KW Human secretory and transmembrane; PRO: mammalian; cancer; lung;  
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
KW adipocyte; A-peptide; factor VIIA; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200140466-A2.  
XX  
PD 07-JUN-2001.  
XX  
PX 01-DEC-2000; 2000WO-US32678.  
XX  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 09-DEC-1999; 99US-0170262.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 30-DEC-1999; 99WO-US31243.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 10-NOV-2000; 2000WO-US30873.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX WPI: 2001-408281/43.  
DR N-PSDB; AAS21288.  
XX  
XX Isolated, secretory and transmembrane PRO polypeptide used to detect  
PT other PRO polypeptides, link bioactive molecules to cells expressing  
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
PT lung, breast, prostate, cervical  
XX  
PS Claim 12; Fig 90; 813pp; English.  
XX  
CC AAU12172-AAU12446 represent novel human secretory and transmembrane  
CC PRO polypeptides. The PRO polypeptides are useful to detect other  
CC PRO polypeptides, to link bioactive molecules to cells expressing  
CC PRO polypeptides, to modulate biological activities of cells expressing  
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
CC polypeptide expression in a cell sample to that in a control sample.  
CC Some of the 275 sequences are also useful to stimulate the release of  
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
CC proliferation or differentiation of chondrocytes, the proliferation or  
CC gene expression in pericyte cells, the release of proteoglycans from  
CC cartilage, the proliferation of inner ear utricular supporting cells or

100

1















DR WPI: 2003-332040/31.  
XX N-PSDB; ACA03647.  
XX New secreted and transmembrane PRO nucleic acids, useful for gene  
PT therapy, in chromosome and gene mapping, as chromosome markers, in  
PT tissue typing, and in chromosome identification  
XX  
XX Claim 12; Fig 90; 660pp; English.  
XX The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The  
CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for  
CC linking bioactive molecules to cells expressing PRO polypeptides,  
CC for modulating biological activities of cells expressing PRO  
CC polypeptides, and for identifying agonists or antagonists.  
CC The PRO polypeptides are useful for stimulating the release of  
CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating  
CC the proliferation or differentiation of chondrocytes, and detecting the  
CC presence of tumours. The polynucleotide sequences encoding PRO  
CC polypeptides are useful as hybridisation probes, in chromosome and  
CC gene mapping, in the generation of antisense RNA and DNA, in the  
CC preparation of PRO polypeptides, for generating transgenic animals or  
CC knockout animals, for the genetic analysis of individuals with genetic  
CC disorders, and in gene therapy. AB066570-AB066844 represent the human  
CC PRO polypeptides of the invention.  
CC Note: The sequence data for this patent was obtained in electronic  
CC format directly from the USPTO web site at  
CC seqdata.uspto.gov/psipsideentry.html.  
XX  
XX Sequence 468 AA;  
SQ

Query Match 99.3%; Score 2384; DB 24; Length 468;  
Best Local Similarity 99.1%; Pred. No. 2.3e-145;  
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGWTWLVLPQAPPGGQSKLNHRELSEAEEDKIKKTYPP 60  
Db 1 MGFLGTGWTWLVLPQAPPGGQSKLNHRELSEAEEDKIKKTYPP 60  
QY 61 ENKPGOSNYSFVDNLNLLRAITEKIEKERSIRSSPLDNKLNVEDVDSTNKRLLIDDY 120  
Db 61 ENKPGOSNYSFVDNLNLLRAITEKIEKERSIRSSPLDNKLNVEDVDSTNKRLLIDDY 120  
QY 121 DSTKSGLDHKFDDPDGLHQLDGTPLTAEDIHVHTAARIYEENDRAVFDKIYSKLLNLGL 180  
Db 121 DSTKSGLDHKFDDPDGLHQLDGTPLTAEDIHVHTAARIYEENDRAVFDKIYSKLLNLGL 180  
QY 181 ITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPTMAAIQDGL 240  
Db 181 ITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPTMAAIQDGL 240  
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Db 241 AKGENDETNSVTLTNGLERTKYSEDNFDFQYFPNFYALLKSIDSEKAKEKETLI 300  
QY 301 TIMKTLIDPVKMWVYIGTISPEGVSYLENLDMALQTKNLEKATNIDNISKLPAPSE 360  
Db 301 TIMKTLIDPVKMWVYIGTISPEGVSYLENLDMALQTKNLEKATNIDNISKLPAPSE 360  
QY 361 KSHEETDSTKEEAARKEKEYGLSKDSTKDDNSNPGKTDPEPKGTEAYLEAIRKNIEWLK 420  
Db 361 KSHEETDSTKEEAARKEKEYGLSKDSTKDDNSNPGKTDPEPKGTEAYLEAIRKNIEWLK 420  
QY 421 KIDKKGKEDYDLSKMRDPIKQADAYVEKGLDKEEAIRKRIYSSL 468  
Db 421 KIDKKGKEDYDLSKMRDPIKQADAYVEKGLDKEEAIRKRIYSSL 468

RESULT 12

AB066890

ID AB066890 standard; Protein; 468 AA.

XX

AC AB066890;  
XX  
XX 27-MAY-2003 (first entry)  
DE Human secreted/transmembrane, PRO, protein SEQ ID 90.  
XX  
KW Human; secreted protein; transmembrane protein; PRO;  
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
KW infertility; birth defects; premature aging; AIDS; biosensor;  
KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
KW bioreactor; tumour.  
XX  
OS Homo sapiens.  
XX US2003032155-A1.  
XX  
XX 13-FEB-2003.  
XX  
XX 03-MAY-2002; 2002US-0137865.  
XX  
XX 31-MAR-1997; 97WO-US05230.  
PR 12-JUN-1998; 98WO-US12456.  
PR 14-JUL-1998; 98WO-US14552.  
PR 28-AUG-1998; 98WO-US17888.  
PR 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19093.  
PR 14-SEP-1998; 98WO-US19094.  
PR 14-SEP-1998; 98WO-US19177.  
PR 16-SEP-1998; 98WO-US19330.  
PR 17-SEP-1998; 98WO-US19437.  
PR 07-OCT-1998; 98WO-US21141.  
PR 29-OCT-1998; 98WO-US22991.  
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PR 20-NOV-1998; 98WO-US24855.  
PR 01-DEC-1998; 98WO-US25108.  
PR 05-JAN-1999; 99WO-US00106.  
PR 08-MAR-1999; 99WO-US05028.  
PR 10-MAR-1999; 99WO-US05190.  
PR 20-APR-1999; 99WO-US08615.  
PR 14-MAY-1999; 99WO-US10733.  
PR 02-JUN-1999; 99WO-US12252.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 05-OCT-1999; 99WO-US21547.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 22-DEC-1999; 99WO-US30720.  
PR 30-DEC-1999; 99WO-US31243.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05746.  
PR 02-MAR-2000; 2000WO-US05841.

PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 22-JUN-2001; 2001WO-US20116.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21738.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 18-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 05-JUN-2001; 2001US-0874503.  
 PR 14-JUN-2001; 2001US-0882636.  
 PR 19-JUN-2001; 2001US-0886342.  
 PR 21-JUN-2001; 2001US-0887879.  
 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.  
 PR (GETH ) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Fillvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI: 2003-331925/31.  
 DR N-PSDB; ACA04068.

XX New secreted and transmembrane nucleic acids and polypeptides,  
 PT designated as PRO, useful for treating inflammation, organ failure,  
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature  
 PT aging, AIDS, or cancer

XX Claim 12; Fig 90; 659pp; English.

XX The invention relates to an isolated nucleic acid comprising, or which is  
 CC at least 80% identical to, or the full-length coding sequence of, any of  
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide  
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid  
 CC further comprises the full-length coding sequence of the DNA deposited  
 CC under American Type Culture Collection (ATCC) accession number in a list  
 CC given in the specification. Also included are vectors and host  
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO  
 CC antibodies, PRO extracellular domains and mature sequences, methods  
 CC of detecting PRO proteins, methods for stimulating the release of

CC TNF-alpha (tumour necrosis factor alpha) from human blood,  
 CC (and the proliferation of differentiation of chondrocyte cells, the  
 CC proliferation of, or gene expression in pericyte cells, the release or  
 CC proteoglycans from cartilage, proliferation of inner ear utricular  
 CC supporting cells, the proliferation of T-lymphocyte cells, the release  
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the  
 CC proliferation of endothelial cells), a method for modulating the uptake  
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,  
 CC or the differentiation of adipocyte cells, a method for factor VITA,  
 CC presence of a tumour in a mammal and an oligonucleotide probe derived  
 CC from any of the nucleotide sequences cited above. The nucleic acids and  
 CC polypeptides are useful for treating inflammatory diseases, organ  
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,  
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or  
 CC diabetic complications. The nucleic acids are useful as hybridisation  
 CC probes, in chromosome and gene mapping, and in generating antisense RNA  
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,  
 CC biosensors or bioreactors. Both are useful in tissue typing.  
 CC The present sequence represents a PRO protein of the invention.

XX Sequence 468 AA;

Query Match 99.3%; Score 2384; DB 24; Length 468;  
 Best Local Similarity 99.1%; Pred. No. 2.3e-145;  
 Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGTTVLVLVLPQAPFKPGSQDKSLHNRELSAERPLNEQIAEEDKIKKTYPP 60  
 DB 1 MGFLGTGTTVLVLVLPQAPFKPGSQDKSLHNRELSAERPLNEQIAEEDKIKKTYPP 60  
 QY 61 ENKPGOSNYSFVDNLLRAITEKIEKERSQSRSSPLDNKLNVEDVDSTNKRKLIDDY 120  
 DB 61 ENKPGOSNYSFVDNLLRAITEKIEKERSQSRSSPLDNKLNVEDVDSTNKRKLIDDY 120  
 QY 121 DSTKSLDHLKFDQDDPDLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIYKSLNLGL 180  
 DB 121 DSTKSLDHLKFDQDDPDLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIYKSLNLGL 180  
 QY 181 ITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENAGKIPKVTMAATQDGL 240  
 DB 181 ITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENAGKIPKVTMAATQDGL 240  
 QY 241 AKGENDETVSNTLTITNGLERTKTYSEDNFRDFOVFPNFFYALLKSIDSEKAKKETLI 300  
 DB 241 AKGENDETVSNTLTITNGLERTKTYSEDNFRDFOVFPNFFYALLKSIDSEKAKKETLI 300  
 QY 301 TIMKTLIDFVKMWKYGTISPPEGVSYLENDEMIALQTKNKKLEKNATDNISKLPAPSE 360  
 DB 301 TIMKTLIDFVKMWKYGTISPPEGVSYLENDEMIALQTKNKKLEKNATDNISKLPAPSE 360  
 QY 361 KSHEETDSTKEEAAKMEKEYGSLKSDTKDDNSNPGGKTDEPKGKTEAVLEATRKNIWLK 420  
 DB 361 KSHEETDSTKEEAAKMEKEYGSLKSDTKDDNSNPGGKTDEPKGKTEAVLEATRKNIWLK 420  
 QY 421 KDKKGNKEDYDLKSMRDFINKQADAYVEKGLDKEEAEAIKRIYSSL 468  
 DB 421 KDKKGNKEDYDLKSMRDFINKQADAYVEKGLDKEEAEAIKRIYSSL 468

RESULT 13  
 ABUS9695

ID ABUS9695 standard; Protein; 468 AA.

XX AC ABUS9695;

XX DT 13-MAY-2003 (first entry)

XX DE Novel secreted and transmembrane protein PRO5990.

XX Human; PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;



KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disorder;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis.

XX Homo sapiens.

XX US2003017563-A1.

XX 23-JAN-2003.

XX 07-MAY-2002; 2002US-0140808.

XX 31-MAR-1997; 97WO-US05230.

XX 12-JUN-1998; 98WO-US12456.

XX 28-AUG-1998; 98WO-US14552.

XX 10-SEP-1998; 98WO-US18824.

XX 14-SEP-1998; 98WO-US19093.

XX 14-SEP-1998; 98WO-US19094.

XX 14-SEP-1998; 98WO-US19177.

XX 16-SEP-1998; 98WO-US19330.

XX 17-SEP-1998; 98WO-US19437.

XX 07-OCT-1998; 98WO-US21141.

XX 29-OCT-1998; 98WO-US22991.

XX 29-OCT-1998; 98WO-US22992.

XX 20-NOV-1998; 98WO-US24855.

XX 01-DEC-1998; 98WO-US25108.

XX 05-JAN-1999; 99WO-US00106.

XX 08-MAR-1999; 99WO-US05028.

XX 10-MAR-1999; 99WO-US05190.

XX 20-APR-1999; 99WO-US08615.

XX 14-MAY-1999; 99WO-US10733.

XX 02-JUN-1999; 99WO-US12252.

XX 01-SEP-1999; 99WO-US20111.

XX 08-SEP-1999; 99WO-US20594.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 05-OCT-1999; 99WO-US23089.

XX 29-NOV-1999; 99WO-US28214.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1999; 99WO-US28301.

XX 01-DEC-1999; 99WO-US28634.

XX 02-DEC-1999; 99WO-US28551.

XX 02-DEC-1999; 99WO-US28564.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 20-DEC-1999; 99WO-US30999.

XX 22-DEC-1999; 99WO-US30720.

XX 30-DEC-1999; 99WO-US31243.

XX 30-DEC-1999; 99WO-US31274.

XX 05-JAN-2000; 2000WO-US00219.

XX 06-JAN-2000; 2000WO-US00277.

XX 06-JAN-2000; 2000WO-US00376.

XX 11-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 18-FEB-2000; 2000WO-US04342.

XX 22-FEB-2000; 2000WO-US04414.

XX 24-FEB-2000; 2000WO-US04914.

XX 24-FEB-2000; 2000WO-US05004.

XX 01-MAR-2000; 2000WO-US05601.

XX 02-MAR-2000; 2000WO-US05746.

XX 02-MAR-2000; 2000WO-US05841.

XX 10-MAR-2000; 2000WO-US06319.

XX 15-MAR-2000; 2000WO-US06884.

XX 20-MAR-2000; 2000WO-US07377.

XX 21-MAR-2000; 2000WO-US07532.

PR 30-MAR-2000; 2000WO-US08439.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 28-JUL-2000; 2000WO-US20710.

PR 11-AUG-2000; 2000WO-US22031.

PR 23-AUG-2000; 2000WO-US23522.

PR 24-AUG-2000; 2000WO-US23328.

PR 08-NOV-2000; 2000WO-US30952.

PR 10-NOV-2000; 2000WO-US30873.

PR 01-DEC-2000; 2000WO-US32678.

PR 20-DEC-2000; 2000WO-US34956.

PR 28-FEB-2001; 2001WO-US06520.

PR 01-MAR-2001; 2001WO-US06666.

PR 25-MAY-2001; 2001WO-US17092.

PR 01-JUN-2001; 2001WO-US17800.

PR 20-JUN-2001; 2001WO-US19692.

PR 22-JUN-2001; 2001WO-US20116.

PR 29-JUN-2001; 2001WO-US21066.

PR 09-JUL-2001; 2001WO-US21735.

PR 20-DEC-2000; 2000US-0747259.

PR 28-FEB-2001; 2001US-0796498.

PR 09-MAR-2001; 2001US-0802706.

PR 14-MAR-2001; 2001US-0808689.

PR 22-MAR-2001; 2001US-0816744.

PR 05-APR-2001; 2001US-0828366.

PR 10-MAY-2001; 2001US-0854208.

PR 18-MAY-2001; 2001US-0854280.

PR 18-MAY-2001; 2001US-0860216.

PR 25-MAY-2001; 2001US-0866028.

PR 25-MAY-2001; 2001US-0866034.

PR 01-JUN-2001; 2001US-0872035.

PR 05-JUN-2001; 2001US-0874503.

PR 14-JUN-2001; 2001US-0882636.

PR 19-JUN-2001; 2001US-0886342.

PR 21-JUN-2001; 2001US-0887879.

PR 18-JUL-2001; 2001US-0908827.

PR 06-AUG-2001; 2001US-0924419.

PR 09-AUG-2001; 2001US-0927796.

PR 16-AUG-2001; 2001US-0931836.

PR 19-DEC-2001; 2001US-0028072.

XX (GETH ) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;

XX WPI; 2003-148238/14.

XX N-PSDB; ABX89185.

XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346

XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes

XX are therapeutically useful for enhancing immune response and in cancer

XX treatments

XX Claim 12; Fig 90; 659pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO

XX polypeptides are useful in detecting PRO polypeptides in a sample, in

XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and

XX in modulating at least one biological activity of a cell expressing a PRO

XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus

XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186

XX stimulate adrenal cortical capillary endothelial growth, and PRO536,

XX PRO943, PRO828, PRO1068 or PRO826, PRO826, PRO819, PRO1126,

XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus

XX useful for treating conditions or disorders where angiogenesis would be

XX beneficial, e.g. wound healing and antagonism of this polypeptide are

XX useful for treating cancerous tumours. PRO812 inhibits vascular

XX endothelial growth factor (VEGF) stimulated proliferation of endothelial

XX cells and is thus useful for inhibiting endothelial cell growth in



241	AKGENDET	V	N	T	L	I	N	G	L	R	T	T	Y	S	E	D	F	E	E	L	Q	T	P	N	F	Y	A	L	L	K	S	I	D	S	E	K	A	K	E	T	L	I		300									
301	TIMKT	L	I	D	F	V	K	M	V	K	Y	G	T	I	S	P	E	G	V	S	Y	L	N	D	E	M	I	A	L	Q	T	K	N	K	L	E	K	N	A	T	N	I	S	K	L	P	A	S	E		360		
301	TIMKT	L	I	D	F	V	K	M	V	K	Y	G	T	I	S	P	E	G	V	S	Y	L	N	D	E	M	I	A	L	Q	T	K	N	K	L	E	K	N	A	T	N	I	S	K	L	P	A	S	E		360		
361	KSHEET	S	T	D	T	K	E	A	A	K	M	E	K	Y	G	S	L	K	D	S	T	K	D	D	S	N	P	G	G	K	T	D	E	P	K	G	T	E	A	L	E	A	I	R	K	N	I	E	W	L	K		420
361	KSHEET	S	T	D	T	K	E	A	A	K	M	E	K	Y	G	S	L	K	D	S	T	K	D	D	S	N	P	G	G	K	T	D	E	P	K	G	T	E	A	L	E	A	I	R	K	N	I	E	W	L	K		420
421	KIDK	G	K	N	K	E	D	Y	L	S	K	M	R	D	F	I	N	K	O	A	D	A	V	E	G	I	L	D	K	E	A	E	A	I	K	R	I	Y	S	S	L		468										
421	KIDK	G	K	N	K	E	D	Y	L	S	K	M	R	D	F	I	N	K	O	A	D	A	V	E	G	I	L	D	K	E	A	E	A	I	K	R	I	Y	S	S	L		468										

RESULT 15

AA013905	AA013905 standard; Protein; 567 AA.
XX	XX
XX	AA013905;
XX	XX
DT	06-NOV-2001 (first entry)
XX	XX
DE	Human polypeptide SEQ ID NO 27797.
XX	XX
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;
KW	nervous system disorders; arthritis; inflammation.
XX	XX
OS	Homo sapiens.
XX	XX
PN	WO200164835-A2.
XX	XX
PD	07-SEP-2001.
XX	XX
PF	26-FEB-2001; 2001WO-US04927.
XX	XX
PR	28-FEB-2000; 2000US-0515126.
PR	18-MAY-2000; 2000US-0577409.
XX	XX
PA	(HYSE-) HYSEQ INC.
XX	XX
PI	Tang YT, Liu C, Drmanac RT;
XX	XX
DR	WPI; 2001-514838/56.
DR	N-PSDB; AA193836.
DR	DR

Query Match: 99.3%; Score 2384; DB 22; Length 567;  
Best Local Similarity 99.1%; Pred. No. 3e-145;

	Matches	464;	Conservative	2;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	MGFLGTCTWILVLP	IOAQPFPKPGSQDKSLHNRELSAERPLNEQIAEAEDKIKKTYPP	60						
Dd	100	MGFLGTCTWILVLP	IOAQPFPKPGSQDKSLHNRELSAERPLNEQIAEAEDKIKKTYPP	159						
Qy	61	ENKPGOSNYSPVDNLNLLRAITKEKETEKERSOTRSSPDLNKLNVEDVDSFNKRKLIDDY	120							
Dd	160	ENKPGOSNYSPVDNLNLLRAITKEKETEKERSOTRSSPDLNKLNVEDVDSFNKRKLIDDY	219							
Qy	121	DSTKSGLDHFKFDDPDGLHQLDGTPLTAEADIVHKIAARIYEENDRAVFDTKVSLLNLGL	180							
Dd	220	DSTKSGLDHFKFDDPDGLHQLDGTPLTAEADIVHKIAARIYEENDRAVFDTKVSLLNLGL	279							
Qy	181	ITSQAHTLDEVAEVLQKLISKANNYEEDPNKPFTSWTENQAQGIPEKVTPMAAIODGL	240							
Dd	280	ITSQAHTLDEVAEVLQKLISKANNYEEDPNKPFTSWTENQAQGIPEKVTPMAAIODGL	339							
Qy	241	AKGENDETVSNTLTTLTNGLERRTKTSYSEDNPDRFOYPNFNVALYKLSIDSEKAKEKETLI	300							
Dd	340	AKGENDETVSNTLTTLTNGLERRTKTSYSEDNFEELQYFPNFYALLKSIDSEKAKEKETLI	399							
Qy	301	TIMKTLLDFVKMMVKYGTISPGEVGSYLENDLEMIALQTNNKLEKNATDNISKLFPPAPSE	360							
Dd	400	TIMKTLLDFVKMMVKYGTISPGEVGSYLENDLEMIALQTNNKLEKNATDNISKLFPPAPSE	459							
Qy	361	KSHETDSTTEEAAMKEKYGSLKSDSTKDONSPPGGTKDEPKGKTEAYLEAIRKNIEWLK	420							
Dd	460	KSHETDSTTEEAAMKEKYGSLKSDSTKDONSPPGGTKDEPKGKTEAYLEAIRKNIEWLK	519							
Qy	421	KHKKGKNKEDYDJSKMRRDFINQADAVVEKGILDKEAAEAIKRIYSSL	468							
Dd	520	KHKKGKNKEDYDJSKMRRDFINQADAVVEKGILDKEAAEAIKRIYSSL	567							

Search completed: August 28, 2003, 10:21:05  
Job time : 72 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	173	7.2	1786	3	US-08-973-462-8	Sequence 8, Appli
2	169.5	7.1	1164	3	US-08-923-992A-2	Sequence 2, Appli
3	169	7.0	1098	3	US-08-923-992A-8	Sequence 8, Appli
4	168	7.0	1164	3	US-08-923-992A-10	Sequence 10, Appli
5	166	6.9	1128	3	US-08-923-992A-6	Sequence 6, Appli
6	165	6.9	1104	3	US-08-923-992A-4	Sequence 4, Appli
7	162.5	6.8	957	4	US-09-914-239-16	Sequence 16, Appli
8	162	6.7	2662	4	US-09-595-684B-31	Sequence 31, Appli
9	158.5	6.6	816	2	US-08-533-306A-6	Sequence 6, Appli
10	158.5	6.6	816	2	US-08-742-923A-6	Sequence 6, Appli
11	158.5	6.6	956	4	US-09-914-239-17	Sequence 17, Appli
12	158	6.6	2285	4	US-09-308-375-2	Sequence 2, Appli
13	157.5	6.6	885	2	US-08-533-306A-4	Sequence 4, Appli
14	157.5	6.6	885	2	US-08-742-923A-4	Sequence 4, Appli
15	155	6.5	1354	3	US-08-685-871-2	Sequence 2, Appli
16	155	6.5	8991	4	US-08-714-741-32	Sequence 32, Appli
17	153.5	6.4	984	1	US-08-242-932-2	Sequence 2, Appli
18	153.5	6.4	984	1	US-08-714-481-2	Sequence 2, Appli
19	153.5	6.4	984	5	PCT-US95-06111-2	Sequence 2, Appli
20	149	6.2	1588	5	PCT-US93-07261-11	Sequence 11, Appli
21	149	6.2	1663	5	PCT-US93-07261-16	Sequence 16, Appli
22	147.5	6.1	1087	4	US-09-914-239-12	Sequence 12, Appli
23	147.5	6.1	1231	4	US-08-714-741-41	Sequence 41, Appli
24	147	6.1	588	4	US-08-714-741-42	Sequence 42, Appli
25	145.5	6.1	864	4	US-08-714-741-40	Sequence 40, Appli
26	145	6.0	534	4	US-09-103-664A-2	Sequence 2, Appli
27	145	6.0	3111	2	US-08-460-309-4	Sequence 4, Appli

Db 1239 ---ISKLEETQELNEVEADLIKONEKLEKALSDESKSDEIDAKDDTLEKVEEHD 1295  
 QY 302 IMKTLIDFVMM-VKYGISPEEGVSYLENDEMIALQTK--NKLEKNATONISKLPAP 358  
 Db 1296 ITTLDVEVELKQVEEDIK---EKVSDLKLEEDILKEVKEKELESEILEDEYKELKTIE 1352  
 QY 359 SEKSHEETDSKEEAAKMEKEVGLSKDSTKDDNSNPGKTDPEPKGTAYLEAIRKNIEW 418  
 Db 1353 TDILEEKEIEKDHPKEFEAEAEIKDLADILAEVSSLEVEEKKLEEVHE-LKEEVEH 1411  
 QY 419 LKKHDK--KGNKEDYDLKMRDINKQADAY---VEKGILDK-----FEARAK 462  
 Db 1412 IISGDAHLKLEED-DLEEVDDLKSGILDMKGMELGDMDKESLEDVTTKLGERVESLK 1470  
 QY 463 RYISS 467  
 Db 1471 DVLSS 1475

## RESULT 2

US-08-923-992A-2  
 ; Sequence 2, Application US/08923992A  
 ; Patent No. 6280738

## GENERAL INFORMATION:

; APPLICANT: Tai, Joseph Y.  
 ; APPLICANT: Blake, Milan S.  
 ; TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms of the Group B  
 ; TITLE OF INVENTION: Streptococcal Beta Antigens  
 ; NUMBER OF SEQUENCES: 34  
 ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

; STREET: 1100 New York Avenue, N.W., Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/923,992A

; FILING DATE: 05-SEP-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/024,707

; FILING DATE: 06-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Esmond, Robert W.

; REGISTRATION NUMBER: 32,893

; REFERENCE/DOCKET NUMBER: 1438.0140001/RWE

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1164 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-923-992A-2

Query Match 7.1%; Score 169.5; DB 3; Length 1164;

Best Local Similarity 21.4%; Pred.No. 0.0003;

Matches 123; Conservative 78; Mismatches 189; Indels 185; Gaps 25;

QY 36 LSAERPLNE-----QIAEAEDEKIKTYPPENKPGQSNYSFVDNLLNLRAT-EKEK 86

Db 149 LELENQFNETNRLHLIKQHEEVEKDKAK-----QKTLKQSDTKVDLSNIDKELNHQSQ 204

QY 87 IEK--ERQSISSPLDNKL-----NVEDVDSTKNRKLIDDYDSTKSGLDHK 130

Db 205 VEKMAEQKGTINEDKDSMLKKIEDIRKQAQADKDEAEVKVREELGKLFSTTRAGLDQE 264  
 QY 131 FODPDGLHQLDGLPTAEDIVHKI-----AARIYEENDRAVEDKIVSKLNLG 179  
 Db 265 IQE-----HVKKET--SSEENTQKDEHYANSLONLAQKSLLELDKATTNEQATQVKNQF 317  
 QY 180 L-----ITESQAHTLEDEVAEV-----LQKLISKE---ANNYEE 210  
 Db 318 LENAQKLEKETOPLIKETNVKLYKAMSELSQVEKELKHNSANLEDLVAKSKEIVREYEG 377  
 QY 211 DPNKPTSWTE-----NOAGKIPEKVTPTMAAIOGLAKGENDETYSN 251  
 Db 378 KLQSKNLPKLQLEEAHSLKQVDEDFRKKFKTSQVTPKRVKRDLANENNQ--Q 434  
 QY 252 TLTITNGLERTKTYSEDNFRDQYFPNFYALLKSIDSEKAKEKETLITIMKTLIDFVK 311  
 Db 435 KIELTVSPENITVEGED-----VKFTVTAKS-DS-----KTTLDPSD 471  
 QY 312 MMVKG--TISPEEGVSYLENLD-----EMIALQTK-----NKLEKNATD 349  
 Db 472 LLTKYNPSVSDRISTNVKNTNDNHKTAETIKNLKLNESQTVILKAKDDSGNVVEKFTTI 531  
 QY 350 NISKLFPAPSEKSHEETDSTKEAA-----KMEKEYGSLKD 385  
 Db 532 TVQKKEEKQVPKTPKQKDSKTEEKVPOEPKSNKQNLQELIKSAQOQLEKLEKAIKELME 591  
 QY 386 STKDDNSNPGKTDPEKGTAEVLAIRKNIEWLKK-----HDKKGKEDYDLKMKRDFIN 441  
 Db 592 Q-PEIPSNP--EYGIQKSIWESQKEPIQEAITSFKKIIGDSSSKSYTYEHFNKYKSDFMN 648  
 QY 442 KQADAYVEKGILDKKEAE-----AIKRIYSS 467  
 Db 649 YQLHAQME--MLTRKVQVYMNKYPDNAEIKKIFES 681

## RESULT 3

US-08-923-992A-8

; Sequence 8, Application US/08923992A

; Patent No. 6280738

; GENERAL INFORMATION:

; APPLICANT: Tai, Joseph Y.

; APPLICANT: Blake, Milan S.

; TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms of the Group B

; TITLE OF INVENTION: Streptococcal Beta Antigens

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

; STREET: 1100 New York Avenue, N.W., Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/923,992A

; FILING DATE: 05-SEP-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/024,707

; FILING DATE: 06-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Esmond, Robert W.

; REGISTRATION NUMBER: 32,893

; REFERENCE/DOCKET NUMBER: 1438.0140001/RWE

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 8:



Query Match	6.9%;	Score 166;	DB 3;	Length 1128;
Best Local Similarity	19.3%;	Pred. No. 0.00051;		
Matches 119;	Conservative 86;	Mismatches 200;	Indels 210;	Gaps 23;

  

QY	25	GSQSKSLNRNLSAERPLNQLAEAEEDKTKTTPPENPGQSNYSF---VDNLLNLRAI	81
Db	69	GKREKQLQWKNLKNVDVNTILSHQKNFKTKIDETVDSDALLELENQFNETNRLLI	128
QY	82	TEKEKIEKERSIRSSL---DNKLNVEDVDTKNR-----K	115
Db	129	KOHEEVEKDKKAKOQKTLKQSDTKVDLSNIDKLNHOKSPVEKMAEPKGIINEDKDSMLK	188
QY	116	LIDD-----YDSTKSLDHLKFODDPDGLHQLDGTPLRAED	150
Db	189	KIEDIRQAQAADKEDAEVKKVREELGKLFSSTKAGLDQE-----IHEHVKETSSEE	241
QY	151	IVHKI-----AARIYEENDRAVPDKTVSKLLNLGL-----	180
Db	242	NTQKVDEHYANSLQNLAQKSLLEEDKATTNQEQVKNQFLENQAOKLKEMOPLIKETNVK	301
QY	181	ITESQAHTLEDEVAEV-----LQKLISKE---ANNYEEDPNKPTSWTE-----	220
Db	302	LYKAMSLSLOVKEKLNHSEANLEOLVAKSKEIVREYEGKLNQSKNLPKLQLEEAHS	361
QY	221	-----NQAGKIPEKTPMAAIOGDLAKENDETYSNTLTITGLNGLERTKTVSDFN	271
Db	362	KLQOVVEDFRKKFTSEQVTPKKRVKRDLAANENQ---QKIETVSPENITVVEGED--	416
QY	272	RDFQYFFNFVALLKSIDSEKAKEKETLITIMKTLIDFVKVMXYG-TISPCEGVSYLEN	330
Db	417	-----VKFTVTAKS-DS-----KTLDFSDLLTKLYNPSVSDRISTNRYKTN	455
QY	331	LD-----EMIALQTK-----NKLEKNATDNISKLPAPSEKSHSEETDST	369



Db 194 KIEDIRKQAQADKEDAEVKVREELKLFSSKAGLDQQIQE-----HVKKET--SSEE 246  
QY 151 IVHKI-----AARIYEENDRAVDFKIVSKLLNLGL----- 180  
Db 247 NTQKVDEHYANSLQNAKSLSELDKATTNEQATQVKNQFLENQAKLKEIQLIKETNVK 306  
QY 181 ITESQAHTLEDEVAEV-----LQKLISKE---ANNYEEDPNKPTSWTE----- 220  
Db 307 LYKAMESLEQVEKELKINSANLQDLVAKSKEIVREYEGKLNOSKNLPELKQLEEEAHS 366  
QY 221 -----NOAGKIPEKVTMAAIOGLAKGENDETVSNLTITLTNGLERRTKYSEDNF 271  
Db 367 KIKQVVEHFKKFTSEQVTPKKRVKRDLANENNQ-----QKIELTVSPENITVYEGED-- 421  
QY 272 RQDFQFPNFPYALLKSIDSEKAKEKETLITIMKTLLIDFVKMMVKY--TISPEEGVSYLEN 330  
Db 422 -----VKFTVTAKS-DS-----KTTLDFSLLTLYNPSVSRISTNYKTN 460  
QY 331 LD-----EMIALQTK-----NKLEKNATDNI-----SKLFPAPSKSHEE 365  
Db 461 TDNHKIAELITIKNLKLNOSQVTLKAKDDSGNVVEKTTITVQKKEEKQVKTPEQKHKS 520  
QY 366 TD-----STKEAAKMEKEYGLSKDSTKDDNSNP---GGKTDEPKG 403  
Db 521 TEQNVQPEPKSNDKNQLOELIKSAQOELEKLEKAIKELMEQ-PEIPSPNPEYGIQKSIWES 579  
QY 404 KTEAYLEAIRKNIEWLKHDKKGNKEDYDLKMRDFINKQADAYVEKGIIDKEAE----- 459  
Db 580 QKEPTQEAITSFNKTIIGDSSSKYTYEHFNKYKSHFMNYQLHAQME--ILTRKVVQYMNK 637  
QY 460 ----AIKRIYSS 467  
Db 638 YPDNAEIRKIPES 650

## RESULT 7

US-09-914-259-16  
; Sequence 16, Application US/09914259  
; Patent No. 6495336  
; GENERAL INFORMATION:  
; APPLICANT: Makowski, Lee  
; APPLICANT: Hyman, Paul  
; APPLICANT: Williams, Mark  
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES  
; FILE REFERENCE: 8471-010-999  
; CURRENT APPLICATION NUMBER: US/09/914,259  
; CURRENT FILING DATE: 2000-11-21  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 957  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-914-259-16

Query Match 6.8%; Score 162.5; DB 4; Length 957;  
Best Local Similarity 19.8%; Pred. No. 0.00075;  
Matches 102; Conservative 96; Mismatches 179; Indels 137; Gaps 23;  
QY 25 GSQKSLHNR-----ELSAERPLNEQIAEAEEDKIKTYPPENKPGQSNYSFVDNLNL-- 78  
Db 321 GORATIKTVSNLELTAE-----ENKKYKEKEKNKTLKNVIOHLEML 367  
QY 79 -----RAITEKEKEKQSRSSPLDNKLNVEDVD-----STKNRKLIDDYDSTKSG 126  
Db 368 NWRNGEAVPEQISAKDQK-NLEPCDNTPIIDNAPVWAGISTEEK---EKYDEEISS 423  
QY 127 LDHKFQDDPDGLHLDGTPLEADIVHKIAARIYEEND-----RAVDFKIVSKLLNLGLI 181  
Db 424 LYRLQDDKDDENQ-----OSQAEKLNQOQMLDQDELLASTRRDYEKIQBELRLQIE 476  
QY 182 TESQAHTLEDEVAEVLOKLISKEANNYE---EDPNKPTSWTENQAGKIPEKVTMAAIOQ 238

Db 477 NEA-----AKDEVKEVLOAL-BELAVNYDOKSOEVEDKTRANEQLTDELAQKTTTLTTTQR 531  
QY 239 GLAK-----GENDETYSNTLTTLNGLERRTKTYSE 268  
Db 532 ELSQLOEVSNHQKRATKILNLLKDLGEIGIIGTND---VKTLDVNGVIEEFTWAR 588  
QY 269 DNFRDQFPNFPYALLKSI-----DSEKEAKEKETLITIMKTLLIDFVKMMVKY 316  
Db 589 -----LYISKMSSEKSLVNRSKQLESQMDSNKMNASERELAACOLLISQHEAKIKS 642  
QY 317 GTISPEEGVSYLENDEMIALQTKNKKLEK---NATDNISKLPAPSEKSHETDSTKE-- 371  
Db 643 LT-----DYMQNM-----QKRQLESQDSISEELAKL--RAQEKMHVSVFQDKEKE 688  
QY 372 -----EAAKMEKEYGLSKDSTKDDNSNPGKTDPEKGTKEAYLEAIRKNIEWLKHDKK 425  
Db 689 HLTRQDAEMKKALEQQMESHREAHQKLSRLDEIBEKQKIIDEIRDLNOKLOEQEK 748  
QY 426 GNKEDYDLKMRDFINKQADAYVEKGIL--DKEE 457  
Db 749 -LSSDYNKLIKIED---QEREMKLEKLLLLNDKRE 778

## RESULT 8

US-09-595-684B-31  
; Sequence 31, Application US/09595684B  
; Patent No. 6544766  
; GENERAL INFORMATION:  
; APPLICANT: Beraud, Christophe  
; APPLICANT: Ohashi, Cara  
; APPLICANT: Sakowicz, Roman  
; APPLICANT: Valsberg, Eugeni  
; APPLICANT: Wood, Kenneth  
; APPLICANT: Yu, Ming  
; TITLE OF INVENTION: Human kinesins and methods of producing  
; and purifying human kinesins  
; FILE REFERENCE: cytop036  
; CURRENT APPLICATION NUMBER: US/09/595,684B  
; CURRENT FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: 09/295,612  
; PRIOR FILING DATE: 2000-04-20  
; NUMBER OF SEQ ID NOS: 105  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 2662  
; TYPE: PRT  
; ORGANISM: Human  
US-09-595-684B-31

Query Match 6.7%; Score 162; DB 4; Length 2662;  
Best Local Similarity 21.6%; Pred. No. 0.0033;  
Matches 118; Conservative 103; Mismatches 176; Indels 150; Gaps 28;  
QY 26 SODKSLHNRSLSAERPLN---EQIAEAEEDKIKTYPPENKPGQSNYSFVDNLNLRAIT 82  
Db 1101 AQEK---NHAIKKEGELSRTCDRLAEVEEKLEKESQQLQKQQL-----LNQVEEMS 1150  
QY 83 EKEKEKEKQSRSSPLDNKLNVEDVDSTK---NRKLIDDYDSTKS-----GLDHHK 130  
Db 1151 EMQKINETENLKNELKNKELTLEHMETERLELAQNLNENYEVKSITKERVYKLELOKS 1210  
QY 131 FODDDPGL---HQLDGTPL-TAEDI---VH-KIAARIYEENDRAVDFKIVSKLLNLGL 180  
Db 1211 FETERDHLRGYITREHATGLQTKKEELKIAHILHKEHQETIDELURRSVSEK-TAQIINTQD 1269  
QY 181 ITESQAHTLEDEVAEVL---QKLIS---KEANNYEEDPNKPTSWTENQAGKIPEKVTMAA 235  
Db 1270 LEKS--HTKLOEIPVLHHEEQELLPNVKVSETQETMNELELLTEOSTTK---DSTTLAR 1324  
QY 236 IQ-----DGLAK-GENDETYSNTL-----TLNGLERRTTK 264  
Db 1325 IEMERLRLNEKFOESQEEIKSLTKERDNLKTIKEALEVHKDQKHEIRETLAKIQESSQK 1384

QY 265 TYSNDRD-----FQYFPNYALLK-----SIDSEKE-AKEKE 297  
 Db 1385 QEQSLNKKEDNETTKIVSEMEQPKPKDSALLRIEIMGLSKRLQSHDMKSVAKED 1444  
 QY 298 TLITIMKTLDIFVKMVKYGTISPGEVSVYLENDEMIA--LOTNNKLE-----KNATD 349  
 Db 1445 DLQRLQEV-----QSESDQLKENKEIVAKHLETEEBELKVAHCCCKRQEE 1490  
 QY 350 NISLFPAPSKSHEETDSTKEEAAKMEKEYGSLKSTKDDNSNPGGKTDEPKKTE--- 406  
 Db 1491 TINELRVNLSEK-----ETEISTIQKLEAINDKLN-----KIQEIYEKEEQLN 1535  
 QY 407 -AYLEARKNIEMWLKHKDKGNKEDYD-----SKMRDFINQADAYVEKGLDKEAEAI 461  
 Db 1536 IKQISEVOENVNLKQPKHKRAKDSALQSTESKMLELTNRLOBSQBEIQIMIKEK-EEM 1594  
 QY 462 KRIYSSL 468  
 Db 1595 KRQVEAL 1601

## RESULT 9

US-08-533-306A-6  
 ; Sequence 6, Application US/08533306A  
 ; Patent No. 5837457  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Pu  
 ; APPLICANT: Collins, Francis S.  
 ; APPLICANT: Siciliano, Michael J.  
 ; APPLICANT: Claxton, David  
 ; TITLE OF INVENTION: Markers for Detection of Chromosome 16  
 ; TITLE OF INVENTION: Rearrangements  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
 ; STREET: P.O. Box 828  
 ; CITY: Bloomfield Hills  
 ; STATE: MI  
 ; COUNTRY: USA  
 ; ZIP: 48303

## COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/533,306A  
 FILING DATE: September 25, 1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Smith, Deann F.  
 REGISTRATION NUMBER: 36683  
 REFERENCE/DOCKET NUMBER: 2115-00869COB  
 TELEPHONE: (810) 641-1600  
 TELEFAX: (810) 641-0270  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 816 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-533-306A-6

Query Match 6.6%; Score 158.5; DB 2; Length 816;  
 Best Local Similarity 22.6%; Pred. No. 0.0012;  
 Matches 110; Conservative 82; Mismatches 186; Indels 109; Gaps 22;

QY 26 SODKSLHNELSRLNFCIAEEDKTKKYPNPKGQSNYSV--DNINLRLAITE 83  
 Db 158 SHREEMENVESVTGMLNE--AEGKAIKLAKDVASLSQLOQTQELLQEBETROKLNVS 215  
 QY 84 KEKIERQSR---SSPLDNKLNVEDVDSTKN-----RKLIDDYDSTKSLGDH---KF 131

Db 216 'LRQLEERNLSIQDQDDEEMAKQNLERHISTNLQLSKSKKLQDFASTVEALEEGKKRF 275  
 QY 132 QDDPDGLHOLDGTPLTAEIDIVHKIAARIYEBENDRAVED-----KIVSKLLNLGLITISQA 186  
 Db 276 QKELENITQOYEEKAAAYDKLETKNRLQQLDLDLVVVDLQNRQLVSNL-----EKKQ 328  
 QY 187 HTLEDEVAEVLQKLISKEANNYEDPNKPTSWTENQAGKIPEKVTMA-AIQDGL-AKGE 244  
 Db 329 RKFOLLAE--EKNIS--SKYADERDR-----AAEAAREKETKALSARALEEAEAKEE 379  
 QY 245 NDETVSNLTLLTNGLERRTKTYSDNFRDFQYFPNFYALLKSIDSDS-----EKEAKEK 296  
 Db 380 LERT-----NKLKAEMED-----LVSSKDDVGVKNVHELEKSKRAL 415  
 QY 297 ETLITIMKTLDIFVKMVKYGTISPGEVSVYLENDEMIALQTKNKLKKNATONISK--- 353  
 Db 416 EQMEEMKTOLEEEDELQ-----ASEDAKLRLVNMQALKGQFEDLQARDEQNEEKRRQ 471  
 QY 354 ----LFPAPSEKSHHEETDSTKEEAAKMEKEYGSLKSTKDDNSNPGGKTDEPK--GKTEA 407  
 Db 472 LQRLHEYTELEDERNERALAAAANKLE-GDLKDLQADSAIKGRERAIKQLRLQA 530  
 QY 408 YLEAIRKNIE-----WLKHKDKGNKEDYDLSKMRDFT-----NKQADAYVEK 450  
 Db 531 QMRDFQRELEDAARASDEIFATAKENEKAKSLEADLMQLQEDLAAAARAKQAD----- 585  
 QY 451 GILDKEE 457  
 Db 586 --LEKEE 590

## RESULT 10

US-08-742-923A-6  
 ; Sequence 6, Application US/08742923A  
 ; Patent No. 5869611  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Pu  
 ; APPLICANT: Collins, Francis S.  
 ; APPLICANT: Siciliano, Michael J.  
 ; APPLICANT: Claxton, David  
 ; TITLE OF INVENTION: Markers for Detection of Chromosome 16  
 ; TITLE OF INVENTION: Rearrangements  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
 ; STREET: P.O. Box 828  
 ; CITY: Bloomfield Hills  
 ; STATE: MI  
 ; COUNTRY: USA  
 ; ZIP: 48303  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/742,923A  
 ; FILING DATE: No. 5869611ember 1, 1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, Deann F.  
 ; REGISTRATION NUMBER: 36683  
 ; REFERENCE/DOCKET NUMBER: 2115-00869DVC  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (810) 641-1600  
 ; TELEFAX: (810) 641-0270  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 816 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein

US-08-742-923A-6

Query Match 6.6%; Score 158.5; DB 2; Length 816;  
Best Local Similarity 22.6%; Pred. No. 0.0012;  
Matches 110; Conservative 82; Mismatches 186; Indels 109; Gaps 22;

QY 26 SODKSLNRELISAERPLNEQIAEEDKIKKTYPPENKPGOSNYSFV--DNLNLLRAITE 83  
DB 158 SHREMEENEVSVTGMLNE--AEGKAIKLAKDVASLSQLODQTOELLQETROKLNSTK 215  
QY 84 KEKTEKROSTR---SSPLDNKLNVEDVSTKN-----RKLIDDYDSTKGLDH---KF 131  
DB 216 LRQLEERNLSQDOLDEMEAKONLERHISTNLQLSDSKKKLQDFASTVALEEGKKRF 275  
QY 132 QDDPDGLHOLDGTPLTAEEDIVHKIAARIYENDRAVFD-----KIVSKLLNGLITESQA 186  
DB 276 QKEIENLTQQYEKAAAYDKLETKNRLQOELDLVVDLQNRQLVSNL-----EKKQ 328  
QY 187 HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPTMA-AIQDGL-ARKE 244  
DB 329 RKFDQLAE--EKNIS---SKYADEROR---AEAEAREKETKALSARALEEAAKEE 379  
QY 245 NDETVSNLTITNGLERRTKTYSEDNFRDFOYFNFVALLKSID-----EKEAKEK 296  
DB 380 LERT-----NKMKAEMED-----LVSSKDDVGKNVHELEKSKRAL 415  
QY 297 ETLITIMKTLLIDFVKMVKYGTISPCEGVSYLENDEMIALQTKNLEKNATDNISK--- 353  
DB 416 ETQMEEMKTQLEEELELQ-----ASEDAKLEVMQALKGOFERDQOARDEQNEKRRQ 471  
QY 354 ---LFPAPSEKSEETDSTKEAAKMEKEVGLSKDSTKDDNSNPGGKTDEPK--GKTEA 407  
DB 472 LQRLHEYTELEDERNERALAAAKKLE-GDLKDLQADSIAKGREAIKQLRKLOA 530  
QY 408 YLEAIRKNIE-----WLKHKDKKNGKDYDLSKMRDFI-----NKQADAYVEK 450  
DB 531 QMKDFQRELEDAARSDIEFAKENEKKAESLEADLMQLEDIAAABERARKQAD----- 585  
QY 451 GILDKKEE 457  
DB 586 --LEKEE 590

RESULT 11

US-09-914-259-17  
; Sequence 17, Application US/09914259  
; Patent No. 6495336  
; GENERAL INFORMATION:  
; APPLICANT: Makowski, Lee  
; APPLICANT: Hyman, Paul  
; APPLICANT: Williams, Mark  
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES  
; FILE REFERENCE: 8471-010-999  
; CURRENT APPLICATION NUMBER: US/09/914,259  
; CURRENT FILING DATE: 2000-11-21  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 956  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-914-259-17

Query Match 6.6%; Score 158.5; DB 4; Length 956;  
Best Local Similarity 20.2%; Pred. No. 0.0015;  
Matches 105; Conservative 89; Mismatches 166; Indels 159; Gaps 25;

QY 25 GSQDKSLNR-----ELSAERPLNEQIAEAEEDKTKTYPPENKPGOSNYSFVDNLLN- 78  
DB 321 GORAKTIKNTVSNLELTAE-----EWKKYKEKEKNAKLSVLQHELMEL 367  
QY 79 -----RAITEKEKE-KEROSIRSSPLDNKLNVED-----VDSTKNRKLIDDYDSTKGL 127

DB 368 NWRNGEAVPEDEQISAKDHKSL--EPCDNTPIIDNITPPVVDGISAER--EKYDEEITSL 423  
QY 128 DHKQDDPDGLHOLDGTPLTAEEDIVHKIAARIYEND-----RAVEDKIVSKLLNGLIT 182  
DB 424 YRQDDDKDDEINQ-----OSQLAEKLOQMLQDDELLASTRRDYEKIQEELRLQIEN 476  
QY 183 ESQAHTLEDEVAEVLQKLISKEANNYE---EDPNKPTSWTENQAGKIPEKVTPTMAAIQDG 239  
DB 477 EA-----AKDEVKEVLQAL-EELAVNYDQKSOEVEDKTRANEQLTDELAQKTTTLTTQRE 531  
QY 240 LAK-----GENDETVSNLTITNGLERRTKTYSED 269  
DB 532 LSQQLSESNHOKKRATEILNLLKDLGIGIGICTND---VKTLADVNGVTEEEFTMAR- 587  
QY 270 NFRDFOYFNPYALLKSI-----DSEKAKEKETLITIMKTLLIDFVKMVKYG 317  
DB 588 -----LYISKMKSEVKSLSVNRSKQLESQMSNRKKNASERELAACQLLISQHEAKIKSL 642  
QY 318 TISPPEGVSYLENDEMIALQTKNLEK---NATDNISKLPAPSEKESHEET--DSTKEE 372  
DB 643 T-----DYQNMW-----QKRRLQESQDSLSSEALAKL--RAQEKMHVSVFQDKEKEH 688  
QY 373 AAKMEKEVGLSKDSTKDDNSNPGGKTDEPKGTAYLEAIRKNIEWLKHDKKNGKEDYD 432  
DB 689 LTRLQ-----DAEEVKALEQQMESHR-----EAHQKQ----- 716  
QY 433 LSKMRDFINKQADAYVEKGILDKKE---EAEAIKRIYSSSL 468  
DB 717 LSRLRDEEEKQRIIDEIRDLNQLQLEQERLSSDYNKL 755

RESULT 12

US-09-308-375-2  
; Sequence 2, Application US/09308375  
; Patent No. 6300117  
; GENERAL INFORMATION:  
; APPLICANT: Genencor  
; TITLE OF INVENTION: Proteases From Gram-Positive Organisms  
; FILE REFERENCE: GC394-PCT  
; CURRENT APPLICATION NUMBER: US/09/308,375  
; CURRENT FILING DATE: 1999-05-14  
; EARLIER APPLICATION NUMBER: EP9719636.4  
; EARLIER FILING DATE: 1997-09-15  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: Bacillus subtilis  
US-09-308-375-2

Query Match 6.6%; Score 158; DB 4; Length 2285;  
Best Local Similarity 23.8%; Pred. No. 0.0033;  
Matches 100; Conservative 61; Mismatches 171; Indels 88; Gaps 16;

QY 85 EKIEKEROISRS--SPLDNKLNVEDVSTKRNKLIDDYDSTKSGLDHKKFQDDPDGLHOLD 142  
DB 1014 DNAKDLQSLLETYSKSDSIDVFKMSFDKAGKNKIDGSKLSVSKSEVGDGELAEAG 1073  
QY 143 GTPLTAEDI-----VHKIAARIYENDRAVFDKIVSKLLNGLITESQAHTLE 190  
DB 1074 N---EAEDFGKKLKEALDANSVDDIKAAIKEMSDAMQFDS--VODVLNGIDFNNT-----K 1124  
QY 191 DEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPTMA---AIQDGLAKGENDE 247  
DB 1125 DQVAP-LNDLLEKMAEG-----KSISANEANTLIQDKELAQAISIENGVVVKINRDE 1175  
QY 248 -----TVSNLTITNGLERRTKTYSEDNFRDFOYFNPYALLKSIDSEK 291  
DB 1176 VIKQKVKLDAYNDVMVTYSNKLUMKTE--VNNALIKTNADTLR-----IDSLK 1220  
QY 292 EAKEKETLITIMKTLLIDF--VKMVKYGTISPCEGVSYLENDEMIALQTKNLEKNATDN 350

Db 1221 KLRKRLDMSAEBSLEVKSINNADAKKE-----LKKLEKMK-----LQPGGYSN 1268  
Qy 351 ISKLFPPAPSEKS-----HEETDSTKEEAAKMEKEYGSLKSTKDDNSNPGKTDPEK 402  
Db 1269 -SQJEAMQVSALEYSISEATSTQEMNKQALVEAGTSLNWTQOQKANEETKYSM 1327  
Qy 403 GKTBAYLEATKNTWELKKHDKGKNGEDYDLSKMRDFINKQADAYVEKGILDKKEEBAIK 462  
Db 1328 YVVDKYEALEKVAEIDKYNQVDPKYSQKYRDAIKKEIKALQOKKKLMQEQAKLLK 1387  
RESULT 13  
US-08-533-306A-4  
; Sequence 4, Application US/08533306A  
; Patent No. 5837457  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Pu  
; APPLICANT: Collins, Francis S.  
; APPLICANT: Siciliano, Michael J.  
; APPLICANT: Claxton, David  
; TITLE OF INVENTION: Markers for Detection of Chromosome 16  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/533,306A  
; FILING DATE: September 25, 1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, DeAnn F.  
; REGISTRATION NUMBER: 36683  
; REFERENCE/DOCKET NUMBER: 2115-00869COB  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810) 641-1600  
; TELEFAX: (810) 641-0270  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 885 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-533-306A-4

Query Match 6.6%; Score 157.5; DB 2; Length 885;  
Best Local Similarity 22.8%; Pred. No. 0.0016;  
Matches 110; Conservative 80; Mismatches 183; Indels 109; Gaps 22;  
Qy 31 LHNRELSAERPLNEQIAEAEDEKIKKTYPPENKPGOSNYSFV--DNLNLLRAITEKEKTE 88  
Db 232 LQNEVESVTGMLE--AEGKAIKADVASLSQLODTQELQOETROKLNSTKLRLQE 289  
Qy 89 KERQSTR---SPSLDNKLNVEDVSTKN-----RKLDDYDSTKSGLDH---KFQDDPD 136  
Db 290 EERNLSQDLDEMEAKQNLERRHISTNLQLSDSKKLQDFASTVEALEEGKRRFKETE 349  
Qy 137 GLHOLDGTPLTAEIDVHKIYAARYENDRAVDF-----KIVSKLLNLGLITESTQALTELD 191  
Db 350 NITQQVEEKAAYDKLEKTKNRLQOELDLVVDLQNRQLVSNL-----EKKQRKFDQ 402  
Qy 192 EYAEVQLKLSKEANNYEEDPNKPTSWTENQAGKIPEKVTPTMA-ATODGL-AKGENDETV 249  
Db 403 LLAE--EKNIS--SKYADERDR---AEAREKXETKALSRLAREALEAKEELERT- 452

Qy 250 SNTLTNLGLERRTKTYSSEDFRDFQYFPNFYALLKKSIDS-----EKEAKKETLIT 301  
Db 453 -----NKMUKAEMED-----LVSSKDDVGKNVHLEKSKRALETOME 489  
Qy 302 IMKTLIDFVMMVKYGTISPEEGVSYLENLDEMIALQTKNKLKKNATDNISK-----L 354  
Db 490 EMKTLQLEBEDELQ-----ASEDAKLRLEVNMQALKGQFDRDLQARDQNEEKRRQLRQL 545  
Qy 355 FPAPSEKSHEETSTKKEAAKMEKEYGSLKSDKDDNSNPGGKTDEPK--GKTPAYLEAI 412  
Db 546 HEYETELEDERNERALAAAKKLE-GDLKDLLELQADSAIKGREEAIKQLRKLQAOAKDF 604  
Qy 413 RKNIE-----WLKKHDKKNGKEDYDLSKMRDFI-----NKQADAYVEKGILDK 455  
Db 605 ORELDARASRDEIFATAKERNKAKSLEADLMQLQEDLAAERARKQAD-----LEK 657  
Qy 456 EE 457  
Db 658 EE 659

RESULT 14  
US-08-742-923A-4  
; Sequence 4, Application US/08742923A  
; Patent No. 5869611  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Pu  
; APPLICANT: Collins, Francis S.  
; APPLICANT: Siciliano, Michael J.  
; APPLICANT: Claxton, David  
; TITLE OF INVENTION: Markers for Detection of Chromosome 16  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: P.O. Box 828  
; CITY: Bloomfield Hills  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 48303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/742,923A  
; FILING DATE: NO. 5869611member 1, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, DeAnn F.  
; REGISTRATION NUMBER: 36683  
; REFERENCE/DOCKET NUMBER: 2115-00869DVC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810) 641-1600  
; TELEFAX: (810) 641-0270  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 885 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-742-923A-4

Query Match 6.6%; Score 157.5; DB 2; Length 885;  
Best Local Similarity 22.8%; Pred. No. 0.0016;  
Matches 110; Conservative 80; Mismatches 183; Indels 109; Gaps 22;  
Qy 31 LHNRELSAERPLNEQIAEAEDEKIKKTYPPENKPGOSNYSFV--DNLNLLRAITEKEKTE 88  
Db 232 LQNEVESVTGMLE--AEGKAIKADVASLSQLODTQELQOETROKLNSTKLRLQE 289

QY 89 KERQSR---SSPLDNKLNVEDVDSTKN-----RKLIDDDYDSTKSGLDH---KFQDDPD 136  
Db 290 EBNLSIQDQDDEMEAKQNLERHISTNLQSDSKKLQDPASTVEALEEGKRFQKEIE 349  
QY 137 GLHOLDGPTLTAEDIVHKIAARIYEENDRAVFD-----KIYSKLNLNLGLITESQAHTLED 191  
Db 350 NITQOYEKAAYDKLETKNRKLOQELDDLVVDLQNRQOLVSNL-----EKKORKFDQ 402  
QY 192 EYAEVLQKLISKEANNYEDPNKPTSWENOAGKIPEKVTMA-AIQDGL-AKGNDETV 249  
Db 403 LLAE--EKNIS--SKYADERD---AEAAREKETALSARALEALEAKELELT- 452  
QY 250 SNTLTLTNGLERRTYSEDNFRDQYFPNFYALKSIDS-----EKAKEKETLIT 301  
Db 453 -----NKMKAEMED-----LVSSKDDVGKNVHELEKSKRALETQME 489  
QY 302 IMKTLIDFVKMVKYGTISPEGVSYLENLDEMIALQTKNLEKNATDNISK-----L 354  
Db 490 EMKTLQLELEDELQ-----ASEDAKLRLVYNMQALKGQFERDQARDEQNEEKRRLQRL 545  
QY 355 FPAPSEKSHETDSTKEEAAMEKEYGSLKDDSTKDDNSNPGGKTDEPK--GKTEAYLEAI 412  
Db 546 HEYTELEDERNERALAAAKKLE--GDLKDLQADSQAIGREAIKQLRKLQAKMDF 604  
QY 413 RKNIE-----WLKHKDKGNKEDYDLKSMRDFI-----NKQADAYVERGILDK 455  
Db 605 QRELEDAASRDEIFATAKENEKAKSLEADLMQLOEDLAAERARKQAD-----LEK 657  
QY 456 EE 457  
Db 658 EE 659

RESULT 15  
US-08-685-871-2  
; Sequence 2, Application US/08685871  
; Patent No. 6013499  
; GENERAL INFORMATION:  
; APPLICANT: NARUMIYA, Shuh  
; APPLICANT: IWAMATSU, Akihiro  
; TITLE OF INVENTION: RHO TARGET PROTEIN KINASE P160  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,871  
; FILING DATE: 24-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 8-184102  
; FILING DATE: 25-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-262553  
; FILING DATE: 14-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 16887/845  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1354 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-685-871-2  
  
Query Match 6.5%; Score 155; DB 3; Length 1354;  
Best Local Similarity 21.0%; Pred. No. 0.0043;  
Matches 104; Conservative 95; Mismatches 181; Indels 116; Gaps 23;  
  
QY 26 SODKSLHNRNLSAERPLNEQIAEA-----ED-----KIKKTYPPNKKPGQSNYSFVDNLN 76  
Db 530 SONSLANEKLS--QLOKQLEANDLLRTESDTAVLRKSHITEMSK-----SISQLESIN 582  
QY 77 LLRAATEKTEKERQSISS--PLDNKNLVEDVDSTKNRKLIDDDYDSTKSGLDHKKFD 133  
Db 583 --RELQERNRILNLSKSTQDKDYQLOAILAEARDRDRHSEMGDLQARITSLOEEVKH 640  
QY 134 DPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLNLNLGLITESQAHTLEDEV 193  
Db 641 LKHNLKVEGERKEAQDMLN-----HSEKEKNLE-----IDLNYKLKLSQORLEQEV 688  
QY 194 AE--VLOKLISKEANNYEE-----DPNKPTSWENOAGKIPEKVTMAAIQ 237  
Db 689 NEHKVTKARLTDKHQSIEEAKSVAMCEMEKKLKEEREAREKAENRVVQI-EKQCSMLD 747  
QY 238 -----DGLAKGENDETIVNTLITNGLERR-----TKTISEDNFRDQYFP 278  
Db 748 LKQSOOKLEHLTGNGKMERMEDEVKNLTQLQESNKRLLQLNELKTOAFEDN----- 799  
QY 279 NFYALLKSIDSEKAKEKETLITIMKTLIDF--VKMVKYGTISPE-----EGVSYL 328  
Db 800 -----LKGL--EKQMKQEIINTLLEAKRLLEFELAQLTQYRGNEGOMRELQDLEAEQYF 852  
QY 329 ENLDEMIALQTKNLEKNATDNISKLFPAPESEKSH-----EETDSTKEEAKE--MEKE 379  
Db 853 STLYKTQVKELKEEIEEKNRENKLTQELQNEKETLATQDLAETKAESQALARGILLEQ 912  
QY 380 YGSL-KDSTKDDNSNPGGKTDEPKGKTEAYLE---AIRKNIEWLKKHDK-----KGNK 428  
Db 913 YFELTQESKKAASRNQREITD--KQHTVSRLEEANSMLTKDIEILLRRENEELTEKMKKAE 970  
QY 429 EDYDLKSMRDFINKQA 444  
Db 971 EYKLEKEEIEISNLKA 986

Search completed: August 28, 2003, 10:25:12  
Job time : 44 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 05:01:52 ; Search time 145 Seconds  
(without alignments)  
6139.792 Million cell updates/sec

Title: US-09-554-945B-1

Perfect score: 2017

Sequence: 1 taaagctacgccttgcgc.....tcaatccttcttcactgtc 2017

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCITUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	86.2	4.3	7218	1	US-08-232-463-14, Appl
2	52.4	2.6	19124	2	US-08-487-826B-13
3	48.8	2.4	3384	3	US-08-923-992A-5
4	48.6	2.4	7218	1	US-08-232-463-14
5	48.2	2.4	2277	1	US-08-676-967-2
6	48.2	2.4	2277	1	US-08-676-974-2
7	48.2	2.4	2277	1	US-09-098-487-2
8	45.6	2.3	2617	1	US-08-430-024-1
9	45.6	2.3	2617	1	US-08-782-009-1
10	45.6	2.3	2617	3	US-09-017-302-1
11	45.6	2.3	3730	1	US-08-242-932-8
12	45.6	2.3	3730	1	US-08-714-481-8
13	45.6	2.3	3730	5	PCT-US95-06111-8
14	45.6	2.3	4200	1	US-08-242-932-1
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17	45.6	2.3	4200	5	PCT-US95-06111-1
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19	43.4	2.2	289	3	US-09-007-005-17
20	43.4	2.2	289	3	US-09-244-796-17
21	43.4	2.2	861	4	US-09-601-198-66
22	43.2	2.1	5361	3	US-08-973-462-2
23	43.2	2.1	6152	3	US-08-973-462-1
24	43	2.1	1436	4	US-08-961-527-327
25	43	2.1	152331	3	US-09-128-155-16
26	42.8	2.1	6755	3	US-08-931-999-4
27	42.4	2.1	754	4	US-09-286-981B-21

Query Match 4.3%; Score 86.2; DB 1; Length 7218;

#### ALIGNMENTS

RESULT 1  
US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: PT99pt-Fls  
US-08-232-463-14

28 42.4 2.1 2081 3 US-08-235-836C-67 Sequence 67, Appl  
29 42.2 2.1 1298 3 US-08-948-705-3 Sequence 3, Appl  
30 42.2 2.1 1298 4 US-09-510-543-3 Sequence 3, Appl  
31 42 2.1 1956 4 US-08-559-896B-1 Sequence 1, Appl  
32 41.8 2.1 2223 1 US-08-257-073-4 Sequence 4, Appl  
33 41.6 2.1 696 3 US-09-461-697-193 Sequence 193, App  
34 41.6 2.1 699 3 US-09-461-697-191 Sequence 191, App  
35 41.6 2.1 717 3 US-09-461-697-189 Sequence 189, App  
36 41.6 2.1 774 3 US-09-461-697-187 Sequence 187, App  
37 41.6 2.1 819 3 US-09-461-697-185 Sequence 185, App  
38 41.6 2.1 1669 3 US-09-461-697-184 Sequence 184, App  
39 41.4 2.1 51952 3 US-08-947-823-1 Sequence 1, Appl  
40 41 2.0 291 1 US-07-922-723A-7 Sequence 7, Appl  
41 41 2.0 291 1 US-07-799-828C-7 Sequence 7, Appl  
42 41 2.0 291 1 US-08-074-275-7 Sequence 7, Appl  
43 41 2.0 291 1 US-08-480-366-7 Sequence 7, Appl  
44 41 2.0 291 2 US-07-952-277A-7 Sequence 7, Appl  
45 40.6 2.0 2427 4 US-09-601-198-70 Sequence 70, Appl

Best Local Similarity 16.8%; Pred. No. 5.3e-13;  
Matches 99; Conservative 243; Mismatches 246; Indels 1; Gaps 1;

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Db 1653 TCTAGATCGACCTGCGAGCAATTCATTTATAGCATAGAAAAACAAATGAAATCTCT-A 1595
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QY 1184 TTACTATCATGAAACACATGATGCTTTGTGAAGATGATGCTGGAATATATGAACAATAT 1243
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QY 1244 CTCAGAGAAGAGTGTTCCTACCTTGAAACTTTGGATGAATGATGCTCTTCAGACCA 1303
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Db 1534 CGCTTCTAGACGCATCTATTCAGTTTCAAAAACGGCATGTAGGCATCACTGTATATACC 1475
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QY 1364 AGAAGATCATGAAGAACACAGACAGTACCAAGGAAGAGAGCTAAGATGGAAGGAAT 1423
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QY 1424 ATGGAAGCTTGAAGGATTCACAAAGATGATACTCCACCCAGGAGGAAAGACAGATG 1483
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Db 1354 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1295
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1484 AACCCAAAGGAAAAACAGAGCCCTATTGGAAGCCATCAGAAAAATATTGAATGGTTGA 1543
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 1604 TCAATAACAGCTGATGCTTATGTGAGAAAGCATCTTGCACAGGAAGAACCGCAGG 1663
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Db 1174 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1115
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QY 1664 CCATCAAGCGCATTTATAGAGCTGTAAAAATGGCAAAAGATCCACGGA 1712
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Db 1114 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1066
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## RESULT 2

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US-08-487-826B-13
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobb Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487.826B
; FILING DATE: 10-SEP-1993
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CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Israelien, Ned  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: NIH121.001CP1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:

LENGTH: 19124 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
US-08-487-826B-13

Query Match 2.68; Score 52.4; DB 2; Length 19124;  
Best Local Similarity 46.7%; Pred. No. 0.0011;  
Matches 199; Conservative 0; Mismatches 226; Indels 1; Gaps 1;

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QY 1212 TGTGAAGATGATGGTGAATATATGGAACAATATCTCCAGAAAGAGTGTTCCTTACCTTGA 1271
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Db 15515 GGAGAAAAATTTTTTAAAAAATAATAAAAAATTTTAAATAATAAAAAATTTTATATA 15574
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QY 1272 AAATCTGGATGAATGATTGCTCTTCAGACCAAAACAACTAGAAAAAATGCTACTGA 1331
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15575 AAAAAATGAAGATTTATCAAAAAAATTTAAAAAATAATAAAAAAATAAAAAAATA 15634
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1332 CAATATAAGCAAGCTTTTCCAGCACCATCAGAGAGAGCTCATGAAGAAACAGACAGTAC 1391
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Db 15635 TTATAAAAAAATAAAAAACAAAAAGAGAAAAAACAATTAAAAAATAAAAAATATAT 15694
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QY 1392 CAAGGAGAGAGCAGCTAAGATGGAAGAAATATGGAAGCTTGAAGG-ATTCCACAAAAG 1450
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Db 15695 ATCATAAAAAACAAAAAATAAAAAAATAATAAAAAAATAAAAAAATAAAAAAATA 15754
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QY 1451 ATGATAACTCCAAACCCAGGAGGAGAGACAGATGAACCCCAAGGAAAAACAGAGCTATT 1510
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Db 15755 AAAAAAATTTAAAAAATGTTAAAAAATAATAATAATAATAATAAAAAAATAAAAA 15814
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QY 1511 TGAAGCCATCAGAAAAAATATTTGAATGTTGAAGAAACATGACAAAAAGGGAAAAATAAG 1570
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Db 15815 TAAATAAAAAAATAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAATA 15874
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QY 1571 AAGATT 1576
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Db 15875 AAAAA 15880
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## RESULT 3

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US-08-923-992A-5
; Sequence 5, Application US/08923992A
; Patent No. 6280738
; GENERAL INFORMATION:
; APPLICANT: Tai, Joseph Y.
; APPLICANT: Blake, Milan S.
; TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms of the Group B
; TITLE OF INVENTION: Streptococcal Beta Antigens
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
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Db 412 GCGCNGTNTYNGARTNAAYATHCCNMGNAARCCNGAYGGNAARATGMNGGNTTYGNN 471  
QY 1423 FATGGAAGCTTGAAGGATCCACAAAAGATGATACTCCACCCAGGAGGAAAGACAGAT 1482  
Db 472 TTYGTNCARTTYAARAYTYNTYNGARGCNGGNAARCCNYTNAARGGNATGAAYATGAAR 531  
QY 1483 GAACCAAGGAAAGAAACAGAGCCCTATTGGAAGCCATCAGAAAAAATATTGAATGGTTG 1542  
Db 532 GARATHAARGGNGMGNACNGTNGCNGTNGAYTGGCNGTNGCNGAYAAARTYAAARGAY 591  
QY 1543 AAGAACAATGACAAAAAGGAAATAAAGAAGATTATGACCTTTCAAAGATGAGAGACTTC 1602  
Db 592 ACNCARWNGTNGMNGCNGNATHGGNGARGAARARWSNCAYGARWSNAARCAICARGARWSN 651  
QY 1603 ATCAATAAACAGCTGATGCTTATGTGAGAGAAAGCCATCCTTGACAAAGGAAGAGCCGAG 1662  
Db 652 GTNAARAARAAGGNGMNGARGARGAYATGGARGARGAARAAYGAYGAYGAY 711  
QY 1663 G 1663  
Db 712 G 712

## RESULT 7

US-09-098-487-2  
; Sequence 2, Application US/09098487  
; Patent No. 5917025  
; GENERAL INFORMATION:  
; APPLICANT: COLLINS, Kathleen  
; TITLE OF INVENTION: Human Telomerase  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Science & Technology Law Group  
; STREET: 268 Bush Street, Suite 3200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/098,487  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Osman Ph.D., Richard A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: UCB96-055  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)343-4341  
; TELEFAX: (415)343-4342  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2277 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-098-487-2

Query Match 2.4%; Score 48.2; DB 2; Length 2277;  
Best Local Similarity 27.8%; Pred. No. 0.0048;  
Matches 167; Conservative 78; Mismatches 356; Indels 0; Gaps 0;  
QY 1063 GAAAGGAGAACTAAACCTACAGTGAACACAACTTTAGGACTTCCATATTTCCCAAT 1122  
Db 112 GARAAGGNGNAAGCTGTGNGGNTTYGNTYAGTNAACNTYWSNATYGTNGARGAY 171  
QY 1123 TTCTATGCGCTACTGAAAGTATTGATTCAGAAAAAGAAAGCAAGAAAAAGAAACACG 1182

Db 172 GTNCARMGNGCNYTNAARGARATHACNACNTTYTGARGGNTGYAARATHAAAYGTNACNGTN 231  
QY 1193 ATTACTATCATGAAAAACACTGATTCGACTTTGTGAAGATGATGGTGAATAATGGAACAATA 1242  
Db 232 GCNAARAARAARYTNGMNAAYAAARACNAARAGARAAGGNAARAAYGARAAVWSNGARTGY 291  
QY 1243 TCTCCAGAGAAGGTGTTTCTTACCTTGAAACTTTGGATGAAATGATTCCTCTTCAGACC 1302  
Db 292 CCNAARAARGARCCNAARCCNAARAARCCNAARNGTNGCNGAYAAARAGCNGMNTNATH 351  
QY 1303 AAAACAAGCTAGAAAAAATGCTACTGACATATATAAGCAAGCTTTTCCAGCAGCATCA 1362  
Db 352 ATHMGAAYTYTWSNTTYAARTGYWSNGARGAYGYTNAARACNGTNTTYGCNCARTTY 411  
QY 1363 GAGAAGACTCATGAAGAACACAGACTACCAAGGAAGAGCAGCTTAAGATGGAAGGAA 1422  
Db 412 GNGCNGTNTYNGARTNAAYATHCCNMGNAARCCNGAYGGNAARATGMNGGNTTYGNN 471  
QY 1423 TATGGAAGCTTGAAGGATTCACAAAAGATGATACTCCACCCAGGAGGAAAGACAGAT 1482  
Db 472 TTYGTNCARTTYAARAYTYNTYNGARGCNGGNAARCCNYTNAARGGNATGAAYATGAAR 531  
QY 1483 GAACCAAGGAAAGAAACAGAGCCCTATTGGAAGCCATCAGAAAAAATATTGAATGGTTG 1542  
Db 532 GARATHAARGGNGMGNACNGTNGCNGTNGAYTGGCNGTNGCNGAYAAARTYAAARGAY 591  
QY 1543 AAGAACAATGACAAAAAGGAAATAAAGAAGATTATGACCTTTCAAAGATGAGAGACTTC 1602  
Db 592 ACNCARWNGTNGMNGCNGNATHGGNGARGAARARWSNCAYGARWSNAARCAICARGARWSN 651  
QY 1603 ATCAATAAACAGCTGATGCTTATGTGAGAGAAAGCCATCCTTGACAAAGGAAGAGCCGAG 1662  
Db 652 GTNAARAARAAGGNGMNGARGARGAYATGGARGARGAARAAYGAYGAYGAY 711  
QY 1663 G 1663  
Db 712 G 712

## RESULT 8

US-08-430-024-1  
; Sequence 1, Application US/08430024  
; Patent No. 5644030  
; GENERAL INFORMATION:  
; APPLICANT: Faulmann, Ervin L  
; TITLE OF INVENTION: NOVEL GENE AND METHOD FOR PRODUCTION OF  
; TITLE OF INVENTION: AN IGA BINDING PROTEIN  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/430,024  
; FILING DATE: 27-APR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/677,209  
; FILING DATE: 29-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: BL-1  
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Streptococcus agalactiae
; STRAIN: DL471
; IMMEDIATE SOURCE:
; CLONE: pELF26
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 320..430
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 320..1510
; OTHER INFORMATION: /codon_start= 320
; OTHER INFORMATION: /function= "binds to Fc region of human IgA"
; OTHER INFORMATION: /product= "IgA binding protein"
; OTHER INFORMATION: /number= 1
; FEATURE:
; NAME/KEY: RBS
; LOCATION: 307..311
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 887..1507
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /bound_moiety= "IgA Fc"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /standard_name= "Human IgA-Fc binding"
; OTHER INFORMATION: /label= IgA-binding
; US-08-430-024-1
;
Query Match 2.3%; Score 45.6; DB 1; Length 2617;
Best Local Similarity 45.3%; Pred. No. 0.026;
Matches 211; Conservative 0; Mismatches 249; Indels 6; Gaps 1;
;
QY 1153 GAAAAAGAACGAGAAAGAACACATGATTACTATCATGAAACACTGATTGACTTT 1212
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; 611 GAAACATCTGCCACTGATCTGGAAACGAGAGAAACATTAACAATGGAAAAATAAT 670
; 1213 GTGAAGATGATGTGAAATATGGAACAATATCTCCAGAAGAGGCTGTTTCTTACCTTGA 1272
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; 671 CTAAAAAATGATGTGCATACACAAATTCCTCATGACAGAAAATGAGTTTAAACA 730
; 1273 AACTTGGATGAATGATGCTCTTCAGACCAAAACAGCTAGAAAAAATGCTACTGAC 1332
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; 731 AAAATTGATGAACAAATGATTCGTGATGATTAGAAATAGAAAATCAATTTAAGGAA 790
; 1333 AATATAAGCAAGCTTTTCCAGCACCATCAGAGAGAGCTCATGAACACACACAGTACC 1392
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; 791 ACTAATAGACTGTACACATCAACAAATGAGAGAGTTGAGAAAGATGAAGAACTAAG 850
; 1393 AAGGAAGAGCAGCTAAGATGGAA-----AAGGAATATGGAAGCTTGAAGGATCCACA 1446
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; 851 CAACAGAAACCTCTGAAACAGTCAGATACGAAAGTAGATCTAAGCAATATTGACAAAG 910
; 1447 AAGATGATACTCAACCCAGGAGGAGAGACAGATGAACCAAGAGGAAAACAGAGGCC 1506
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
; 911 CTTATCATCAAAAAGTCAAGTTGAAAAAATGGCAGAGCAAAAGGGAATCACAATGAA 970
; 1507 TATTGGAGCCATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAAT 1566
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; 971 GATAAAGATTCATGCTGAAAAAATCGAAGATATTCGTAACACAGCTCAACAGCAGAT 1030
; 1567 AAGAAGATATGACCTTCAAGATGAGAGACTTCATCAATAAAC 1612
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Db 1031 AAAAAAGAGATCCGGAAGTAAGGTTCTGTAAGAACTAGTAAAC 1076
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RESULT 9
; US-08-782-009-1
; Sequence 1, Application US/08782009
; Patent No. 5714334
; GENERAL INFORMATION:
; APPLICANT: Faulmann, Ervin L
; TITLE OF INVENTION: NOVEL GENE AND METHOD FOR PRODUCTION OF
; AN IgA BINDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/782,009
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,024
; FILING DATE: 27-APR-1995
; APPLICATION NUMBER: US 07/677,209
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: BL-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus agalactiae
; STRAIN: DL471
; IMMEDIATE SOURCE:
; CLONE: pELF26
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 320..430
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 320..1510
; OTHER INFORMATION: /codon_start= 320
; OTHER INFORMATION: /function= "binds to Fc region of human IgA"
; OTHER INFORMATION: /product= "IgA binding protein"
; OTHER INFORMATION: /number= 1
; FEATURE:
; NAME/KEY: RBS
; LOCATION: 307..311
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 887..1507
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /bound_moiety= "IgA Fc"
; OTHER INFORMATION: /evidence= EXPERIMENTAL

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Qy	1447	AAAGATGATTAAC	TCCAAACCCAGGAGGAAAGACAGATGAACCCAAAGAAACAGAGCC	1506
Db	721	CTTAATCATCA	AAAAAAGTCAAGTTGAAAAAATGCGACAGCAAAAGGGAATCACAAAATGAA	780
Qy	1507	TATTTGAAGCCAT	CAGAAAAAATATTGAATGCTTGNAGAAAGCATGACAAAAAGGGAAT	1566
Db	781	GATAAGAGATTCT	ATGCTGTAAGAAAAATCGAAGATATTTCGTAAACAAGCTCAACAGCAGAT	840
Qy	1567	AAAGAAGATTAT	TACCTTTTCAAGATGAGAGACTTTCATCAATAAAC	1612
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RESULT 12  
 US-08-714-481-8  
 ; Sequence 8, Application US/08714481  
 ; Patent No. 5766606  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brady, L. Jeannine  
 ; TITLE OF INVENTION: Cloning of No. 5766606-IgA Fc Binding Forms of  
 ; TITLE OF INVENTION: The Group B Streptococcal Beta Antigens  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Saliwanchik & Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: FL  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/714,481  
 ; FILING DATE: 16-SEP-1996  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/242,932  
 ; FILING DATE: 16-MAY-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saliwanchik, David R.  
 ; REGISTRATION NUMBER: 31,794  
 ; REFERENCE/DOCKET NUMBER: UFI142  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 904-375-8100  
 ; TELEFAX: 904-372-5800  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3730 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-714-481-8

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; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3730 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
US-08-714-481-8

Query Match      2.3%;   Score 45.6;   DB 1;   Length 3730;
Best Local Similarity 45.3%;   Pred. No. 0.031;
Matches 211;   Conservative 0;   Mismatches 249;   Indels 6;   Gaps 1;

QY      1153  GAAAGAAGCAAAAGACAAACACTGATTACTATCATGAAACACTGATTGACTTT 1212
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Db      421  GAACATCTGCCATGATCTGGAAACGAGAGAAACAATTTACAACAATGGAAAAATAAT 480
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QY      1213  GTGAAGATGATGGTGAAATATGGACAATATCTCCAGAAGAAGGTGTTTCCCTACCTGAA 1272
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Db      481  CTAATAAATGATGTGGATAACACAATTCATCTCATGAACAGAAANAATGACTTTAAACA 540
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QY      1273  AACITGGATGAATGATTGCTTCTCAGACACAAAACAAAGCTAGAAAAAATGCTACTGAC 1332
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Db      541  AAAATTGTAACACAATGATCTCGATTTATAGAATTTAGAAAAATCAATTTAAGGAA 600
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REFERENCE/DOCKET NUMBER: UF142

Search completed: August 28, 2003, 08:26:05  
Job time : 147 secs





; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/125778  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/125826  
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; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: PCT/US01/21735  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 80  
; SEQ ID NO 66  
; LENGTH: 1893  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-331-836-66

Query Match 92.5%; Score 1866.4; DB 11; Length 1893;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
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Db 1 GTCTCCGCGTCACAGCAACTTCAGCACCCACAGGGCGGACAGCGTCCCTCTTACTCTGA 60  
QY 82 GACTTGACTCCCGCGCGCCCAACCTGCTTATCCCTTGACCGTGCAGTGTGAGATCC 141  
Db 61 GACTTGACTCCCGCGCGCCCAACCTGCTTATCCCTTGACCGTGCAGTGTGAGATCC 120  
QY 142 TGCAGCGCGCCAGTCCCGCGCCCTCTCCCGCCCCACACCCACCTCTGGCTTCTTCTGT 201  
Db 121 TGCAGCGCGCCAGTCCCGCGCCCTCTCCCGCCCCACACCCACCTCTGGCTTCTTCTGT 180  
QY 202 TTTTACTCTCTCTTTTTCATTATACAAAGCTACAGTCCAGAGCCAGCGCGGGCT 261  
Db 181 TTTTACTCTCTCTTTTTCATTATACAAAGCTACAGTCCAGAGCCAGCGCGGGCT 240  
QY 262 GTGACCCAAAGCGAGCGTGGAGAAATGGGGTTCCCTCGGACCGGCACCTTGGATTCTGTG 321  
Db 241 GTGACCCAAAGCGAGCGTGGAGAAATGGGGTTCCCTCGGACCGGCACCTTGGATTCTGTG 300  
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Db 301 TTAGTGTCTCCGATTCAAGCTTTTCCCAAACTGGAGGAAGCCAAAGAAATCTCTACAT 360  
QY 382 AATAGAGAAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAAGAC 441  
Db 361 AATAGAGAAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAAGAC 420  
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Db 421 AAGATTAAAAAACATATCTCCAGAAAAAAGCCAGGTCCAGAGCAACTATTCTTTTGT 480  
QY 502 GATAACTTGAACCTGCTAAGGGCAATACAGAAAAAGGAAAAATGAGAAAGAAAGCAA 561  
Db 481 GATAACTTGAACCTGCTAAGGGCAATACAGAAAAAGGAAAAATGAGAAAGAAAGCAA 540  
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Db 541 TCTATAAGAGCTCCCACTTTGATTAATGAATGTGAAGATGTGATTTCAACCAAG 600  
QY 622 AATCGAAACTGATCGATGATTGACTCTACTAAGAGTGGATGGATATAAATTTCAA 681  
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Db 661 GATGATCCAGATGGTCTTTCATCAACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTC 720

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Db 721 CATAAATCGCTCCAGATTTATGAAGAAATGACAGAGCGGTGTTGGACAAGATTGTT 780  
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Db 781 TCTAACTACTTAATCTCGGCTTATCAGAGAGCCAGCAGACATACACTGGAAGATCAA 840  
QY 862 GTAGCAGAGGTTTACAAAATTAATCTCAAGAGGAGCCAACTATATGAGGAGGATCCC 921  
Db 841 GTAGCAGAGGTTTACAAAATTAATCTCAAGAGGAGCCAACTATATGAGGAGGATCCC 900  
QY 922 AATAGCCCAAGCTGACTGAGAAATCAGGCTGGAAAAATACAGAGAAAGTCACTCCA 981  
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Db 1081 GAATCCCAATATTTCCCAATTTCTATCGGCTACTGAAAGTATTTGATTCAGAAAAAGAA 1140  
QY 1162 GCRAAGAGAAAGAACACTGATTACTATCATGAAACACTGATTGTTGTAAGATG 1221  
Db 1141 GCAAGAGAAAGAAACACTGATTACTATCATGAAACACTGATTGTTGTAAGATG 1200  
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QY 1402 GCACCTAAGATGGAAGGAATATGGAAGCTTGAAGATTCACAAAAGATGATACTCC 1461  
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QY 1762 TCTGTGATTAATAATTTTTCAGCCCAAGGGTTATTAGAAAGTGCCTGAATTTACAGTACTTA 1821  
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RESULT 2

US-10-035-977-66  
; Sequence 66, Application US/10035977  
; Publication No. US20030134327A1  
; GENERAL INFORMATION:  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3030R1C10  
; CURRENT APPLICATION NUMBER: US/10/035,977  
; CURRENT FILING DATE: 2001-12-26  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/112514  
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Db 1801 ACCTTTTACAGTGGTTAAACATAGCTTTCTCCCGTAAAAAACTATCTGAAAGTAAAGT 1860  
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; PRIOR APPLICATION NUMBER: PCT/US01/21066
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; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 66
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-035-977-66

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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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61  GACTTGACTCCCGCGCGCCCAACCCCTGCTTATCCCTTGACCCGTGAGTGTCTCAGAGATCC 120
QY      142  TGCAGCGCGCCAGTCCCGCGCCCTCTCCCGCCCCACACCCCTCTCTGGCTCTTCTGCTGT 201
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121  TGCAGCGCGCCAGTCCCGCGCCCTCTCCCGCCCCACACCCCTCTCTGGCTCTTCTGCTGT 180
QY      202  TTTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 261
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181  TTTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY      262  GTGACCCAAAGCGAGCGTGGAAAGTGGGTTCTCTCGGACCGGCGACTTTGGATTTCTGGTG 321
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241  GTGACCCAAAGCGAGCGTGGAAAGTGGGTTCTCTCGGACCGGCGACTTTGGATTTCTGGTG 300
QY      322  TTAGTGTCTCCGATTCAGCTTTCCCAACCTCGAGGAGCCAGACAAATCTCTACAT 381
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301  TTAGTGTCTCCGATTCAGCTTTCCCAACCTCGAGGAGCCAGACAAATCTCTACAT 360
QY      382  AATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAAGAAAGAC 441
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361  AATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAAGAAAGAC 420
QY      442  AAGATTAAGAAACATATCTCCAGAAACAGGCGAGGTGAGAGCAATATTCTTTGTT 501
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421  AAGATTAAGAAACATATCTCCAGAAACAGGCGAGGTGAGAGCAATATTCTTTGTT 480
QY      502  GATAACTTGAACCTGCTAAGGGCAATAACAGAAAAAGAAAAATTTGAGAAAGAAAGACAA 561
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481  GATAACTTGAACCTGCTAAGGGCAATAACAGAAAAAGAAAAATTTGAGAAAGAAAGACAA 540
QY      562  TCTATAAGAGCTCCCACTTTGATAATAGTTGAATGTGAAGATGTTGATTTCACACCAAG 621
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541  TCTATAAGAGCTCCCACTTTGATAATAGTTGAATGTGAAGATGTTGATTTCACACCAAG 600
QY      622  AATCGAAACATGATCGATGATTATGACTCTACTAAGAGTGGATGGATCATATAATTTCAA 681
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601  AATCGAAACATGATCGATGATTATGACTCTACTAAGAGTGGATGGATCATATAATTTCAA 660
QY      682  GATGATCCAGATGGTCTTTCATCAACTAGACGGGACTCCTTTAAGCGGTGAAGACATGTC 741
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661  GATGATCCAGATGGTCTTTCATCAACTAGACGGGACTCCTTTAAGCGGTGAAGACATGTC 720
QY      742  CATAAATCGCTGCCAGATTTATGAAGAAATCAGAGCCGTGTTTGACAAGATGTT 801
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721  CATAAATCGCTGCCAGATTTATGAAGAAATCAGAGCCGTGTTTGACAAGATGTT 780
QY      802  TCTAAACTACTTAATCTCGGCTTTATCAGAGAAAGCAAGCACATACACTGGAAGATGAA 861
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781  TCTAAACTACTTAATCTCGGCTTTATCAGAGAAAGCAAGCACATACACTGGAAGATGAA 840
QY      862  GTAGCAGAGTTTACAAAAATTAATCTCAAGGAGCCCAACAATTAAGAGGAGGATCCC 921
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841  GTAGCAGAGTTTACAAAAATTAATCTCAAGGAGCCCAACAATTAAGAGGAGGATCCC 900
QY      922  AATAGCCCAACAGCTGAGTGAATCAGCTGGAATAATACAGAGAAAGTGAAGTCACTCCA 981
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901  AATAGCCCAACAGCTGAGTGAATCAGCTGGAATAATACAGAGAAAGTGAAGTCACTCCA 960
QY      982  ATGCGAGCAATCAAGATGCTTTGCTTAAGGAGAAACAGATGAACAGATGATCTAACACA 1041
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961  ATGCGAGCAATCAAGATGCTTTGCTTAAGGAGAAACAGATGAACAGATGATCTAACACA 1020
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|||||
1021  TTAACCTTGACAAATGCTTGGAAAGAGAGAACTTAAACCTACAGTGAAGACAACTTTAGG 1080
QY      1102  GACTTCCAAATATTCCCAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAAAAAGAA 1161
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QY 1282 GAATGATGCTCTTCAGACCAAAACACAGCTAGAAAAATGCTACTGACAAATATAGC 1341  
Db 1261 GAATGATGCTCTTCAGACCAAAACACAGCTAGAAAAATGCTACTGACAAATATAGC 1320  
QY 1342 AAGCTTTTCCAGCACCATCAGAGAGAGTATGAAGAAACAGACAGTACCAAGGAAGAA 1401  
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QY 1402 GCAGTAAAGTGAAGAAAGATATGGAAGCTTTGAAGATTCACAAAAAGATGATACTCC 1461  
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QY 1762 TCTGTGATTAATAATTTTGGCCCAAGGGTTATTAGAAAGTGTCTGAATTTACAGTAGTTA 1821  
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Db 1801 ACCTTTTACAGTGGTTAAACATAGCTTTCTTCCCGTAAAAACATATCTGAAAGTAAAGT 1860  
QY 1882 TGTATGTAAGCTGAGA 1897  
Db 1861 TGTATGTAAGCTGAAA 1876

RESULT 3  
US-10-063-735-149  
; Sequence 149, Application US/10063735  
; Publication No. US20030138882A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3230R1C1  
; CURRENT APPLICATION NUMBER: US/10/063,735

; CURRENT FILING DATE: 2002-05-08  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 149  
; LENGTH: 1893  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; US-10-063-735-149  
  
Query Match 92.5%; Score 1866.4; DB 12; Length 1893;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 22 GTCTCCGGGTACAGAGAACTTCAGACACCCACAGGCGGACAGCGTCCCTCTACCTGGA 81  
Db 1 GTCTCCGGGTACAGAGAACTTCAGACACCCACAGGCGGACAGCGTCCCTCTACCTGGA 60  
QY 82 GACTTGACTCCGCGCGCCCAACCTGCTTATTCCTTTCAGCGTGCAGTGTGAGATCC 141  
Db 61 GACTTGACTCCGCGCGCCCAACCTGCTTATTCCTTTCAGCGTGCAGTGTGAGATCC 120  
QY 142 TGCAGCGCCAGTCCCGGCCCTCTCCGCGCCCAACCTGCTTATTCCTTTCAGCGTGCAGTGTGAGATCC 201  
Db 121 TGCAGCGCCAGTCCCGGCCCTCTCCGCGCCCAACCTGCTTATTCCTTTCAGCGTGCAGTGTGAGATCC 180  
QY 202 TTTTACTCTCTCTTTTTCATTATACAAAAAGCTACAGCTCCAGGAGCCCGCGCGGT 261  
Db 181 TTTTACTCTCTCTTTTTCATTATACAAAAAGCTACAGCTCCAGGAGCCCGCGCGGT 240  
QY 262 GTGACCCAGCGCGGTGGAAGATGGGGTTCTCGGACCGGCACCTTGGATTCGTGGT 321  
Db 241 GTGACCCAGCGCGGTGGAAGATGGGGTTCTCGGACCGGCACCTTGGATTCGTGGT 300  
QY 322 TTAGTCTCCCGATTCAAGCTTTCCCAACCTTGGAGGAGCCAGACAAATCTCTACAT 381  
Db 301 TTAGTCTCCCGATTCAAGCTTTCCCAACCTTGGAGGAGCCAGACAAATCTCTACAT 360  
QY 382 AATAGAGAAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTCGTAAGCAGAAAGAC 441  
Db 361 AATAGAGAAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTCGTAAGCAGAAAGAC 420  
QY 442 AAGATTAAAAACATATCTCCAGAAACAGCCAGGTGAGAGCACTTCTTTTGT 501  
Db 421 AAGATTAAAAACATATCTCCAGAAACAGCCAGGTGAGAGCACTTCTTTTGT 480  
QY 502 GATTAAGTCAAGCTCTTAAGGCAATAACAGAAAGGAAATTCAGAAAGAAAGACAA 561  
Db 481 GATTAAGTCAAGCTCTTAAGGCAATAACAGAAAGGAAATTCAGAAAGAAAGACAA 540  
QY 562 TCTATAAGAGTCCCGACTTTGATATAAGTTGAATGTGAAGATGTTGATTCACCAAG 621  
Db 541 TCTATAAGAGTCCCGACTTTGATATAAGTTGAATGTGAAGATGTTGATTCACCAAG 600  
QY 622 AATCGAAAACTGATCGATGATTAAGTCTACTAAGAGTGGATTTGATCATAAATTCAA 681  
Db 601 AATCGAAAACTGATCGATGATTAAGTCTACTAAGAGTGGATTTGATCATAAATTCAA 660  
QY 682 GATGATCCAGATGCTTTCATCACTAGACGGAGCTTTCCTTAAACCGCTGACAGCATGTC 741  
Db 661 GATGATCCAGATGCTTTCATCACTAGACGGAGCTTTCCTTAAACCGCTGACAGCATGTC 720  
QY 742 CATATAATCGCTCCAGGATTTTATGAAGAAATTCAGAGCGGTGTTTGAAGATGTTT 801  
Db 721 CATATAATCGCTCCAGGATTTTATGAAGAAATTCAGAGCGGTGTTTGAAGATGTTT 780  
QY 802 TCTAACTACTTAATCTCGGCTTATACAGAAAGCCAGACATACACTGGAAGATGAA 861  
Db 781 TCTAACTACTTAATCTCGGCTTATACAGAAAGCCAGACATACACTGGAAGATGAA 840  
QY 862 GTAGCAGAGGTTTACAAAAATTAATCTCAAGAGGAGCCAAATATATGAGGAGATCC 921  
Db 841 GTAGCAGAGGTTTACAAAAATTAATCTCAAGAGGAGCCAAATATATGAGGAGATCC 900

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QY 922 AATAAGCCACAAAGCTGGACTGAGAAATACAGGCTGGAAGAAATACAGAGAAAGTGAATCCCA 981
Db 901 AATAAGCCACAAAGCTGGACTGAGAAATACAGGCTGGAAGAAATACAGAGAAAGTGAATCCCA 960
QY 982 ATGGCAGCAATTAAGATGGTCTTCTAAGGAGAAACGATGAACAGTATCTAACAACA 1041
Db 961 ATGGCAGCAATTAAGATGGTCTTCTAAGGAGAAACGATGAACAGTATCTAACAACA 1020
QY 1042 TTAACCTTTGACAAATGGCTTGGAAAGGAGAACTTAAACCTTACAGTGAAGACAACTTTAGG 1101
Db 1021 TTAACCTTTGACAAATGGCTTGGAAAGGAGAACTTAAACCTTACAGTGAAGACAACTTTAGG 1080
QY 1102 GACTTCCCAATATTTCCCAAAATTTCTATCGCTACTGAAAGATATGATTCAGAAAAAGAA 1161
Db 1081 GAATCCCAATATTTCCCAAAATTTCTATCGCTACTGAAAGATATGATTCAGAAAAAGAA 1140
QY 1162 GCAAAAGAGAAAGAAACACTGATTACTATCATGAAACACACGATGACTTTGTGAAGATG 1221
Db 1141 GCAAAAGAGAAAGAAACACTGATTACTATCATGAAACACACGATGACTTTGTGAAGATG 1200
QY 1222 ATGGTGAATATGGAACAATATCTCCAGAAAGAGTGTCTTCTACCTTGAACAACTTGGAT 1281
Db 1201 ATGGTGAATATGGAACAATATCTCCAGAAAGAGTGTCTTCTACCTTGAACAACTTGGAT 1260
QY 1282 GAAATGATGCTCTTCAGACCAAAACAAAGCTGAAAGAAATGCTACTGACAAATATAAGC 1341
Db 1261 GAAATGATGCTCTTCAGACCAAAACAAAGCTGAAAGAAATGCTACTGACAAATATAAGC 1320
QY 1342 AAGCTTTTCCAGCACCACATCAGAGAAGAGTATCATGAAGAAACAGACAGTACCAAGGAGAA 1401
Db 1321 AAGCTTTTCCAGCACCACATCAGAGAAGAGTATCATGAAGAAACAGACAGTACCAAGGAGAA 1380
QY 1402 GCAGCTAAGATGGAAGAAATATGGAAGCTTGAAGATTTCCACAAAGATGATTAAGTCC 1461
Db 1381 GCAGCTAAGATGGAAGAAATATGGAAGCTTGAAGATTTCCACAAAGATGATTAAGTCC 1440
QY 1462 AACCCAGGAGAAAGACAGATGAACCCAAAGGAAACACAGAGCTTATTTGGAAGCCATC 1521
Db 1441 AACCCAGGAGAAAGACAGATGAACCCAAAGGAAACACAGAGCTTATTTGGAAGCCATC 1500
QY 1522 AGAAAAATATGAATGGTTGAAGAAACATGACAAAAAGGAAATAAAGAAATATGATGAC 1581
Db 1501 AGAAAAATATGAATGGTTGAAGAAACATGACAAAAAGGAAATAAAGAAATATGATGAC 1560
QY 1582 CTTTCAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTGGAAGAAAGCATC 1641
Db 1561 CTTTCAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTGGAAGAAAGCATC 1620
QY 1642 CTTGACAAAGGAAGACCGAGGCCATCAAGCGCATTTATAGCAGCCCTGTAAAGAAAGGCAA 1701
Db 1621 CTTGACAAAGGAAGACCGAGGCCATCAAGCGCATTTATAGCAGCCCTGTAAAGAAAGGCAA 1680
QY 1702 AAGATCCAGAGTCTTTCAACTGTTTCAAGAAACATATATAGCTTTAAACACTTCTAAT 1761
Db 1681 AAGATCCAGAGTCTTTCAACTGTTTCAAGAAACATATATAGCTTTAAACACTTCTAAT 1740
QY 1762 TCTGTGATTAATAATTTTGAACCCAGGCTTATAGAAAGTGTGAATTTACAGTAGTTA 1821
Db 1741 TCTGTGATTAATAATTTTGAACCCAGGCTTATAGAAAGTGTGAATTTACAGTAGTTA 1800
QY 1822 ACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCGTAAGAAACTATCTGAAAGTAAAGT 1881
Db 1801 ACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCGTAAGAAACTATCTGAAAGTAAAGT 1860
QY 1882 TGTATGTAAGCTGAGA 1897
Db 1861 TGTATGTAAGCTGAGA 1876

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RESULT 4  
 US-10-137-870-89  
 : Sequence 89, Application US/10137870  
 : Publication No. US20030138883A1

```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerriksen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C155
; CURRENT APPLICATION NUMBER: US/10/137,870
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 89
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-137-870-89

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Query Match 92.5%; Score 1866.4; DB 12; Length 1893;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 GTCTCCGCTCACAGGAACCTTCAGCACCCACAGGGCGGAGCGCTCCCTCTTACCTGGA 81
Db 1 GTCTCCGCTCACAGGAACCTTCAGCACCCACAGGGCGGAGCGCTCCCTCTTACCTGGA 60
QY 82 GACTTGACATCCCGCGCGCCCAACCTGCTTATCCCTTACCGTGCAGTGTGAGATCC 141
Db 61 GACTTGACATCCCGCGCGCCCAACCTGCTTATCCCTTACCGTGCAGTGTGAGATCC 120
QY 142 TGCAGCGCGCCAGTCCCGCGCCCTCTCCCGCCCGCCACACACCCCTCTTCCCTGCTTCCCTG 201
Db 121 TGCAGCGCGCCAGTCCCGCGCCCTCTCCCGCCCGCCACACACCCCTCTTCCCTGCTTCCCTG 180
QY 202 TTTTACTCTCTCTTTTCAATTCATATACAAAGCTACAGTCTCCAGAGCCCGCGCGGCT 261
Db 181 TTTTACTCTCTCTTTTCAATTCATATACAAAGCTACAGTCTCCAGAGCCCGCGCGGCT 240
QY 262 GTGACCCAGCGCGGAGGAGTGGGTTCCTCCGGACCGGCGGCTTGGATTCGTTG 321
Db 241 GTGACCCAGCGCGGAGGAGTGGGTTCCTCCGGACCGGCGGCTTGGATTCGTTG 300
QY 322 TTAGTGTCTCCGATTCAGAGCTTTCCCAAACTGGAGGAGCAAGACAAATCTCTACAT 381
Db 301 TTAGTGTCTCCGATTCAGAGCTTTCCCAAACTGGAGGAGCAAGACAAATCTCTACAT 360
QY 382 AATAGAGAAATTAAGTGCAGAAAGACCTTTTGAATGAACAGATTTGCTGAAAGCAAGAAC 441
Db 361 AATAGAGAAATTAAGTGCAGAAAGACCTTTTGAATGAACAGATTTGCTGAAAGCAAGAAC 420
QY 442 AAGATTAATAAATAATATCTCCAGAAACAGGCGGCTCAGACCACTATCTTTGTT 501
Db 421 AAGATTAATAAATAATATCTCCAGAAACAGGCGGCTCAGACCACTATCTTTGTT 480
QY 502 GATAACTTGAACCTGCTTAAGGCAATTAACAGAAAGGAAAAAATTTGAGAAAAAGACAA 561
Db 481 GATAACTTGAACCTGCTTAAGGCAATTAACAGAAAGGAAAAAATTTGAGAAAAAGACAA 540
QY 562 TCTATAAGAGCTCCCGCACTTGATTAAGTTGAATGTGGAAGATGTTGATTCAACCAAG 621
Db 541 TCTATAAGAGCTCCCGCACTTGATTAAGTTGAATGTGGAAGATGTTGATTCAACCAAG 600

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Db 541 TCTATAAGAGCTCCCCACTTGATATAAAGTTGAATGTGGAAGATGTTGATTCAACCAAG 600  
QY 622 AATCGAAACATGATCGATGATATGACCTCTACTAAGAGTGGATGGATCATATAATTTCAA 681  
Db 601 AATCGAAACATGATCGATGATATGACCTCTACTAAGAGTGGATGGATCATATAATTTCAA 660  
QY 682 GATGATCCAGATGGTCTTCATCAACTAGACGGGACTCCTTTAACCGCTGGAAGACATGTC 741  
Db 661 GATGATCCAGATGGTCTTCATCAACTAGACGGGACTCCTTTAACCGCTGGAAGACATGTC 720  
QY 742 CATAAATTCGCTGCCAGGATTTATCAAGAAATGACAGAGCCGCTGTTTGACAAGATGTT 801  
Db 721 CATAAATTCGCTGCCAGGATTTATCAAGAAATGACAGAGCCGCTGTTTGACAAGATGTT 780  
QY 802 TCTAACTACTTAATCTCGGCTTATACAGAAAGCCAAAGCACATACACTGGAAGATGAA 861  
Db 781 TCTAACTACTTAATCTCGGCTTATACAGAAAGCCAAAGCACATACACTGGAAGATGAA 840  
QY 862 GTAGCAGAGTTTACAAAATTAATCTCAAGGAAGCCAAATATGAGGAGGATGCC 921  
Db 841 GTAGCAGAGTTTACAAAATTAATCTCAAGGAAGCCAAATATGAGGAGGATGCC 900  
QY 922 AATAGCCCAAGCTGACCTGAGATCAGCTGGAATAATACCAGAGAAAGTGACTCCA 981  
Db 901 AATAGCCCAAGCTGACCTGAGATCAGCTGGAATAATACCAGAGAAAGTGACTCCA 960  
QY 982 ATGCAGCAATTCAGATGGTCTTGCTAAGGAGAAACAGTGAACAGTATCTAACACA 1041  
Db 961 ATGCAGCAATTCAGATGGTCTTGCTAAGGAGAAACAGTGAACAGTATCTAACACA 1020  
QY 1042 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTAAACCTACAGTGAAGACACTTTAGG 1101  
Db 1021 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTAAACCTACAGTGAAGACACTTTAG 1080  
QY 1102 GACTTCCAAATATTCACAAATTTCTATCGCTACTGAAAGTATTTGATTCAGAAAAGAA 1161  
Db 1081 GAATCCCAATATTCACAAATTTCTATCGCTACTGAAAGTATTTGATTCAGAAAAGAA 1140  
QY 1162 GCAAAAGAGAAGAAACACTGATTACTATCATGAAACACTGATTGACTTTGTGAAGATG 1221  
Db 1141 GCAAAAGAGAAGAAACACTGATTACTATCATGAAACACTGATTGACTTTGTGAAGATG 1200  
QY 1222 ATGTTGAATATGGAACAATATCTCCAGAAAGAGTGTTCCTACCTTGAACACTTGGAT 1281  
Db 1201 ATGTTGAATATGGAACAATATCTCCAGAAAGAGTGTTCCTACCTTGAACACTTGGAT 1260  
QY 1282 GAAATGATGCTCTTCAGACCAAAACAAAGCTAGAAAATATGCTACTGACAAATATAGC 1341  
Db 1261 GAAATGATGCTCTTCAGACCAAAACAAAGCTAGAAAATATGCTACTGACAAATATAGC 1320  
QY 1342 AAGCTTTTCCAGACCATCATCAGAGAAGTCTATGAAGAAACAGACAGTACCAAGGAAGAA 1401  
Db 1321 AAGCTTTTCCAGACCATCATCAGAGAAGTCTATGAAGAAACAGACAGTACCAAGGAAGAA 1380  
QY 1402 GCAGTAAATGGAAGGAATATGGAAGTGAAGATTCACAAAGATGATACTCC 1461  
Db 1381 GCAGTAAATGGAAGGAATATGGAAGTGAAGATTCACAAAGATGATACTCC 1440  
QY 1462 AACCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAGCTATTTTGAAGCCATC 1521  
Db 1441 AACCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAGCTATTTTGAAGCCATC 1500  
QY 1522 AGAAAAATATTTGAATGGTTGAAGAAACATGACAAAAAGGGAATAAAGAAAGATATGAC 1581  
Db 1501 AGAAAAATATTTGAATGGTTGAAGAAACATGACAAAAAGGGAATAAAGAAAGATATGAC 1560  
QY 1582 CTTTCAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTTGGAAGAAAGGCATC 1641  
Db 1561 CTTTCAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTTGGAAGAAAGGCATC 1620  
QY 1642 CTTGACAGGAAGAACCGGAGCCATCAAGCGCATTTATAGCAGCCGTGTAATAATGGCAA 1701  
Db 1621 CTTGACAGGAAGAACCGGAGCCATCAAGCGCATTTATAGCAGCCGTGTAATAATGGCAA 1680

QY 1702 AAGATCCAGGAGTCTTTCAACTGTTTCAAGAAACATAATATAGCTTAAAAACACTTCTAAT 1761  
Db 1681 AAGATCCAGGAGTCTTTCAACTGTTTCAAGAAACATAATATAGCTTAAAAACACTTCTAAT 1740  
QY 1762 TCTGTGATTAATAATTTTTTGACCCCAAGGGTTATTAGAAGTCTGAAATTTACAGTAGTTA 1821  
Db 1741 TCTGTGATTAATAATTTTTTGACCCCAAGGGTTATTAGAAGTCTGAAATTTACAGTAGTTA 1800  
QY 1822 ACCTTTTACAAGTGGTTAAAAACATAGCTTTCTCCCGTAAAAACCTATCTGAAAGTAAAGT 1881  
Db 1801 ACCTTTTACAAGTGGTTAAAAACATAGCTTTCTCCCGTAAAAACCTATCTGAAAGTAAAGT 1860  
QY 1882 TGTATGTAAGCTGAGA 1897  
Db 1861 TGTATGTAAGCTGAAA 1876

## RESULT 5

US-10-140-018-89  
; Sequence 89, Application US/10140018  
; Publication No. US20030138885A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330RIC158  
; CURRENT APPLICATION NUMBER: US/10/140,018  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 89  
; LENGTH: 1893  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-140-018-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 22 GTCTCCGCGTCACAGGAATCTTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGA 81  
Db 1 GTCTCCGCGTCACAGGAATCTTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGA 60  
QY 82 GACTTGACTCCCGCGCGCCCAACCTGCTTATCCCTTTGACCGTGCAGTGTGACAGATCC 141  
Db 61 GACTTGACTCCCGCGCGCCCAACCTGCTTATCCCTTTGACCGTGCAGTGTGACAGATCC 120  
QY 142 TGCAGCGCCGACGTCGCCGCCCTCTCCGCCCCACACCCCTCTCTGGCTCTTCTCTGT 201  
Db 121 TGCAGCGCCGACGTCGCCGCCCTCTCTCCGCCCCACACCCCTCTCTGGCTCTTCTCTGT 180  
QY 202 TTTTACTCCTCTCTTTCATTATCAACAAAGCTACAGTCCAGGAGCCCGCGGCT 261  
Db 181 TTTTACTCCTCTCTTTCATTATCAACAAAGCTACAGTCCAGGAGCCCGCGGCT 240



QY	262	GTGACCCAAACCGAGCGTGAAGAATGGGGTTCTCGGACCGGCACTTGGATTTCTGGTG	321
DB	241	GTACCCAAAGCCGAGGTGGAAATGGGTTCTCGGACCGGCACTTGGATTTCTGGTG	300
QY	322	TTAGTGTCTCCCGATTCAAGCTTTCCCCAAACCTGGAGGAGCCAAAGACAAATCTCTACAT	381
DB	301	TTAGTGTCTCCCGATTCAAGCTTTCCCCAAACCTGGAGGAGCCAAAGACAAATCTCTACAT	360
QY	382	AATAGAGAAATTAAGTCAGAAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAAGAAC	441
DB	361	AATAGAGAAATTAAGTCAGAAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAAGAAC	420
QY	442	AGATTAAAAAACAATATCCTCCAGAAAACAGCCAGGTTCAGAGCAATTTCTTTTGGTT	501
DB	421	AGATTAAAAAACAATATCCTCCAGAAAACAGCCAGGTTCAGAGCAATTTCTTTTGGTT	480
QY	502	GATAACTTGAACCTGCTAAGGGCAATTAACAGAAAAGGAAAAAATTTGAGAAAACAAAGACAA	561
DB	481	GATAACTTGAACCTGCTAAGGGCAATTAACAGAAAAGGAAAAAATTTGAGAAAACAAAGACAA	540
QY	562	TCTATAAGAAAGCTCCCACTTGTATTAATAGTTGAATGTGGAAGATGTTGATTCACACCAAG	621
DB	541	TCTATAAGAAAGCTCCCACTTGTATTAATAGTTGAATGTGGAAGATGTTGATTCACACCAAG	600
QY	622	AATCGAAAACTGATCGATGATTATGACTCTACTTAAGAGTGGATTGGATCATATAAATTTCAA	681
DB	601	AATCGAAAACTGATCGATGATTATGACTCTACTTAAGAGTGGATTGGATCATATAAATTTCAA	660
QY	682	GATGATCCAGATGGTCTTCATCACTAGACGGGACTCCTTTAAACCGCTGAAGACATTGTC	741
DB	661	GATGATCCAGATGGTCTTCATCACTAGACGGGACTCCTTTAAACCGCTGAAGACATTGTC	720
QY	742	CATAAAATCGCTGCCAGGATTTATCAAGAAAATGACAGCGCTGTTTGGACAAGATTGTT	801
DB	721	CATAAAATCGCTGCCAGGATTTATCAAGAAAATGACAGCGCTGTTTGGACAAGATTGTT	780
QY	802	TCTAAACTACTTAATCTCGGCTTTATCACAGAAAGCCCAAGCACATACACTGGAAGATGAA	861
DB	781	TCTAAACTACTTAATCTCGGCTTTATCACAGAAAGCCCAAGCACATACACTGGAAGATGAA	840
QY	862	GTAGCAGAGGTTTTACAAAAATTAATCTCAAGGAAGCCCAACAATTTATGAGGAGATCCC	921
DB	841	GTAGCAGAGGTTTTACAAAAATTAATCTCAAGGAAGCCCAACAATTTATGAGGAGATCCC	900
QY	922	AATAGCCCAACAGGTGACATGAGATCAGGCTGGAAAAATACCAGAGAAAGTGACTCCA	981
DB	901	AATAGCCCAACAGGTGACATGAGATCAGGCTGGAAAAATACCAGAGAAAGTGACTCCA	960
QY	982	ATGGCAGCAATTCAGATGGTCTTGCTAAGGAGAAAACAGTGAACAGATATCTTAACACA	1041
DB	961	ATGGCAGCAATTCAGATGGTCTTGCTAAGGAGAAAACAGTGAACAGATATCTTAACACA	1020
QY	1042	TTAACCCTTGACAAATGGCTTGGAAAGGAGAACTAAAAACCTACAGTGAAGACAACTTTAGG	1101
DB	1021	TTAACCCTTGACAAATGGCTTGGAAAGGAGAACTAAAAACCTACAGTGAAGACAACTTTAGG	1100
QY	1102	GACTTCCAAATATTTCCCAAAATTTCTATGCGCTACTGAAAAGTATTGATTCAGAAAAAGAA	1161
DB	1081	GACTTCCAAATATTTCCCAAAATTTCTATGCGCTACTGAAAAGTATTGATTCAGAAAAAGAA	1140
QY	1162	GCAAAAGAGAAAGAAACACTGATTACTATCATGAAAAACACTGATTGACTTTGTGAAGATG	1221
DB	1141	GCAAAAGAGAAAGAAACACTGATTACTATCATGAAAAACACTGATTGACTTTGTGAAGATG	1200
QY	1222	ATGGTGAATATGAAACAATATCTCCAGAGAAAGGTGTTTCCTTACCTTGAAAACTTTGGAT	1281
DB	1201	ATGGTGAATATGAAACAATATCTCCAGAGAAAGGTGTTTCCTTACCTTGAAAACTTTGGAT	1260
QY	1282	GAAATGATTGCTCTTTCAGACCAAAAACAACTAGAAAAAAATGCTACTGACAATATAAGC	1341
DB	1261	GAAATGATTGCTCTTTCAGACCAAAAACAACTAGAAAAAAATGCTACTGACAATATAAGC	1320
QY	1342	AAGCTTTTCCACACCATCAGAGAGATGTCATGAAGAAACAGACAGTACCAAGGAAGAA	1401

[illegible]

## RESULT 6

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: US/10-140-021-89
: Sequence 89, Application US/10140021
: Publication No. US2003013886A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Flisaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Collin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRADE
: TITLE OF INVENTION: ACIDS ENCODING
: FILE REFERENCE: P330R1C167
: CURRENT APPLICATION NUMBER: US/10/140-
: CURRENT FILING DATE: 2002-05-06
: Prior Application removed - See Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 89
: LENGTH: 1893
: TYPE: DNA
: ORGANISM: Homo Sapien

```



US-10-140-021-89

Query Match		92.5%;	Score 1866.4;	DB 12;	Length 1893;		
Best Local Similarity		99.7%;	Pred. No. 0;				
Matches 1870;		Conservative	0;	Mismatches	6;	Indels	0; Gaps 0;
QY	22	GTCTCCGCTCACAGAACTT	CAGACCCACAGCGCGGACAGCGCTCCCTCTACCTGGA	81			
DB	1	GTCTCCGCTCACAGAACTT	CAGACCCACAGCGCGGACAGCGCTCCCTCTACCTGGA	60			
QY	82	GACTTGACTCCGCGCGCCCA	CCCTGCTTATCCCTTGACCGTGCAGTGTCCAGATCC	141			
DB	61	GACTTGACTCCGCGCGCCCA	CCCTGCTTATCCCTTGACCGTGCAGTGTCCAGATCC	120			
QY	142	TGCAGCGCCAGTCCGCGCCCT	CTCCGCGCCACACCCCTCCCTGCTTCTTCTGT	201			
DB	121	TGCAGCGCCAGTCCGCGCCCT	CTCCGCGCCACACCCCTCCCTGCTTCTTCTGT	180			
QY	202	TTTTACTCCTCTTTTTCAT	ATCATAAAGCTACAGTCTCCAGAGCCGCGCGGCT	261			
DB	181	TTTTACTCCTCTTTTTCAT	ATCATAAAGCTACAGTCTCCAGAGCCGCGCGGCT	240			
QY	262	GTGACCCAGCGAGCGTGG	AGATGGGTTCCTCGGACCGGCACCTTGGATTCTGGTG	321			
DB	241	GTGACCCAGCGAGCGTGG	AGATGGGTTCCTCGGACCGGCACCTTGGATTCTGGTG	300			
QY	322	TTAGTGCTCCCGATTCA	AGCTTCCCAAACTGGAGGAGCAACAAATCTCTACAT	381			
DB	301	TTAGTGCTCCCGATTCA	AGCTTCCCAAACTGGAGGAGCAACAAATCTCTACAT	360			
QY	382	AATGAGAAATTAAGTGC	AGAAAGCCTTTGAATGAACAGATGTCTGAAAGCAAGAAC	441			
DB	361	AATGAGAAATTAAGTGC	AGAAAGCCTTTGAATGAACAGATGTCTGAAAGCAAGAAC	420			
QY	442	RAGATTAATAAACAAT	ATCCTCCCAAAACAGCCAGCTCAGCAACTATCTTTTGT	501			
DB	421	RAGATTAATAAACAAT	ATCCTCCCAAAACAGCCAGCTCAGCAACTATCTTTTGT	480			
QY	502	GATAACTTGAACCTGCT	AGGGCAATAACAGAAAGGAAAAATTTGAGAAAGAAAGACAA	561			
DB	481	GATAACTTGAACCTGCT	AGGGCAATAACAGAAAGGAAAAATTTGAGAAAGAAAGACAA	540			
QY	562	TCTATAAGAGCTCCCA	CTTGAATTAAGTGAATGGAAGATGTGATTCACCAAG	621			
DB	541	TCTATAAGAGCTCCCA	CTTGAATTAAGTGAATGGAAGATGTGATTCACCAAG	600			
QY	622	AATCGAAACTGATCG	ATGATGATGAGTGGATTCATATAAATTTCAA	681			
DB	601	AATCGAAACTGATCG	ATGATGATGAGTGGATTCATATAAATTTCAA	660			
QY	682	GATGATCCAGATGGT	CTTCACTAGACGGGACTCTTTAACCGCTGAAGACATTTGC	741			
DB	661	GATGATCCAGATGGT	CTTCACTAGACGGGACTCTTTAACCGCTGAAGACATTTGC	720			
QY	742	CATAAAATCGCTCC	AGGATTTATGAAGAAATGACAGCGCGTCTTTGACAAGATGTT	801			
DB	721	CATAAAATCGCTCC	AGGATTTATGAAGAAATGACAGCGCGTCTTTGACAAGATGTT	780			
QY	802	TCTAACTACTTAAT	CTCGGCTTATCAGAGAAACCAAGCATACACTGGAAGATGAA	861			
DB	781	TCTAACTACTTAAT	CTCGGCTTATCAGAGAAACCAAGCATACACTGGAAGATGAA	840			
QY	862	GTAGCAGAGGTTT	TACAAAAATTAATCTCAAGAGGAGCCCAACAATATGAGGAGGATCCC	921			
DB	841	GTAGCAGAGGTTT	TACAAAAATTAATCTCAAGAGGAGCCCAACAATATGAGGAGGATCCC	900			
QY	922	AATAAGCCCAAGCT	GGACTGGAAATCAGGCTGGAAAAATACCAGAGAAAGTGTACTCCA	981			
DB	901	AATAAGCCCAAGCT	GGACTGGAAATCAGGCTGGAAAAATACCAGAGAAAGTGTACTCCA	960			
QY	982	ATGGCAGCAATTC	AGATGGTCTTCTAGGGAGAAAAACGATGAAACAGTATCTAACACA	1041			
DB	961	ATGGCAGCAATTC	AGATGGTCTTCTAGGGAGAAAAACGATGAAACAGTATCTAACACA	1020			

QY	1042	TTAACCCTTGACAAATGG	CTTGAAAGGAGAACTTAAACCTACAGTGAAGACAACCTTAGG	1101			
DB	1021	TTAACCCTTGACAAATGG	CTTGAAAGGAGAACTTAAACCTACAGTGAAGACAACCTTAGG	1080			
QY	1102	GACTTCCCAATATTTCC	CAAAATTTCTATGGCTACTGAAAGATTTGATTCAGAAAAAGAA	1161			
DB	1081	GAACTTCCAATATTTCC	CAAAATTTCTATGGCTACTGAAAGATTTGATTCAGAAAAAGAA	1140			
QY	1162	GCAAAGAGAAAGAAC	ACTGATTAATCATGAAACACTGATTGACTTTCTGGAAGTG	1221			
DB	1141	GCAAAGAGAAAGAAC	ACTGATTAATCATGAAACACTGATTGACTTTCTGGAAGTG	1200			
QY	1222	ATGCTGAAATATGGA	CAACATATCTCCAGAAGAGTGTTCCTACCTTGAAACCTTGGAT	1281			
DB	1201	ATGCTGAAATATGGA	CAACATATCTCCAGAAGAGTGTTCCTACCTTGAAACCTTGGAT	1260			
QY	1282	GAAATGATTCCTTC	CAGACCAAAACAAAGCTAGAAAAAATGCTACTGCAATATAAGC	1341			
DB	1261	GAAATGATTCCTTC	CAGACCAAAACAAAGCTAGAAAAAATGCTACTGCAATATAAGC	1320			
QY	1342	AACTTTTCCCAAG	CACTCAGAGAGTCTATGAAGAACACAGACTACCAAGGAAGAA	1401			
DB	1321	AACTTTTCCCAAG	CACTCAGAGAGTCTATGAAGAACACAGACTACCAAGGAAGAA	1380			
QY	1402	CGAGCTAAGATG	GAAAGGAATATGGAAGCTTTGAAGGATTCACAAAAAGATGATACTCC	1461			
DB	1381	CGAGCTAAGATG	GAAAGGAATATGGAAGCTTTGAAGGATTCACAAAAAGATGATACTCC	1440			
QY	1462	AACCCAGGAGG	AAAGACAGATGAACCCAAAGGAAACAGAGCCCTATTTGGAAGCCATC	1521			
DB	1441	AACCCAGGAGG	AAAGACAGATGAACCCAAAGGAAACAGAGCCCTATTTGGAAGCCATC	1500			
QY	1522	ACAAAAATATTA	ATGATGTTGAAGAAACATGACAAAGGAGAAATAAGAAAGATATGAC	1581			
DB	1501	ACAAAAATATTA	ATGATGTTGAAGAAACATGACAAAGGAGAAATAAGAAAGATATGAC	1560			
QY	1582	CTTTCAAGATG	AGAGCTTCATCAATAAACAGCTGATGCTTATGTGGAGAAAGGCATC	1641			
DB	1561	CTTTCAAGATG	AGAGCTTCATCAATAAACAGCTGATGCTTATGTGGAGAAAGGCATC	1620			
QY	1642	CTTGACAGG	AAAGACCCGAGCCATCAAGCCGCTTATAGCAGCCCTGTAAAAATGGCAA	1701			
DB	1621	CTTGACAGG	AAAGACCCGAGCCATCAAGCCGCTTATAGCAGCCCTGTAAAAATGGCAA	1680			
QY	1702	AAAGTCCAG	AGCTTTTCAACTGTTTCAGAAAAACATAATATAGCTTAAAAACACTTCTAAT	1761			
DB	1681	AAAGTCCAG	AGCTTTTCAACTGTTTCAGAAAAACATAATATAGCTTAAAAACACTTCTAAT	1740			
QY	1762	TCGTGATTA	AAATTTTGGACCCAGGGTTATTAGAAAAGTCTGATTTTACAGTAGTTA	1821			
DB	1741	TCGTGATTA	AAATTTTGGACCCAGGGTTATTAGAAAAGTCTGATTTTACAGTAGTTA	1800			
QY	1822	ACCTTTTACA	AGTGGTTAAAAACATAGCTTTTCCCGTAAAAACATATCTGAAAGTAAAGT	1881			
DB	1801	ACCTTTTACA	AGTGGTTAAAAACATAGCTTTTCCCGTAAAAACATATCTGAAAGTAAAGT	1860			
QY	1882	TGATGTA	AGCTTCAGA 1897				
DB	1861	TGATGTA	AGCTTCAGA 1876				

RESULT 7  
US-10-140-274-89  
; Sequence 89, Application US/10140274  
; Publication NO. US20030143674A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C161  
CURRENT APPLICATION NUMBER: US/10/140,274  
CURRENT FILING DATE: 2002-05-06  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 89  
LENGTH: 1893  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-140-274-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	22	GTCTCCGCGTCACAGGAACCTTACAGCACCCACAGCGGCGAGCGCTCCCTCTACCTGGA	81
DB	1	GTCTCCGCGTCACAGGACTTACAGCACCCACAGCGGCGAGCGCTCCCTCTACCTGGA	60
QY	82	GACTTGACTCCCGCGGCCCAACCTCTGCTTATCCCTTGACCGCTCGAGTGTACAGATCC	141
DB	61	GACTTGACTCCCGCGGCCCAACCTCTGCTTATCCCTTGACCGCTCGAGTGTACAGATCC	120
QY	142	TGACGCGCCGCTCCCGGCCCTCTCCGCCCCACACCCCTCTGCTGCTTCCCTGT	201
DB	121	TGACGCGCCGCTCCCGGCCCTCTCCGCCCCACACCCCTCTGCTGCTTCCCTGT	180
QY	202	TTTTACTCTCTCTTTTCATTCATACAAAGCTTACAGCTCCAGAGCCCGCCGCGGT	261
DB	181	TTTTACTCTCTCTTTTCATTCATACAAAGCTTACAGCTCCAGAGCCCGCCGCGGT	240
QY	262	GTACCCCAAGCCGAGCGTGAAGATGGGGTTCCTCGGACCGGCACTTTGGATTCGGTG	321
DB	241	GTACCCCAAGCCGAGCGTGAAGATGGGGTTCCTCGGACCGGCACTTTGGATTCGGTG	300
QY	322	TTAGTGCTCCCGATTCAAGCTTTCCCAAACTTGGAGGAGCCCAAGCAAACTCTACAT	381
DB	301	TTAGTGCTCCCGATTCAAGCTTTCCCAAACTTGGAGGAGCCCAAGCAAACTCTACAT	360
QY	382	ATAGAGAAATTAAGTCGAGAAAGACCTTTGAATGAACAGATTCGTTGAAGCAAGAAC	441
DB	361	ATAGAGAAATTAAGTCGAGAAAGACCTTTGAATGAACAGATTCGTTGAAGCAAGAAC	420
QY	442	AAGATTAAGAAACATATCTCCAGAAACACAGCCAGGTCAGAGCACTATTCTTTGTT	501
DB	421	AAGATTAAGAAACATATCTCCAGAAACACAGCCAGGTCAGAGCACTATTCTTTGTT	480
QY	502	GATACTTTGAACCTGCTAAGGGCAATAACAGAAAAAGGAAAAAATTTGAGAAAAAGACAA	561
DB	481	GATACTTTGAACCTGCTAAGGGCAATAACAGAAAAAGGAAAAAATTTGAGAAAAAGACAA	540
QY	562	TCATTAAGAGCTCCCGCTTGTATATAGTTGAATGTGGAAGATGTTGATTCACCAAG	621
DB	541	TCATTAAGAGCTCCCGCTTGTATATAGTTGAATGTGGAAGATGTTGATTCACCAAG	600
QY	622	AATCGAAACTGATCGATGATTAAGCTTACTTACAGAGTGGATGGATCATAAATTTCAA	681
DB	601	AATCGAAACTGATCGATGATTAAGCTTACTTACAGAGTGGATGGATCATAAATTTCAA	660
QY	682	GATGATCCAGATGGTCTTTCATCACTACAGCGGACTCCCTTTAACCGCTGAAGACATTGTC	741

DB	661	GATGATCCAGATGGTCTTTCATCACTAGAGGGGACTCCTTTAAGCGCTGAAGACATTGTC	720
QY	742	CATAAAATCGCTGCCAGGATTTATGAAGAAATACAGAGCCGTTGTTGACAGATGTT	801
DB	721	CATAAAATCGCTGCCAGGATTTATGAAGAAATACAGAGCCGTTGTTGACAGATGTT	780
QY	802	TCATAACTACTTAACTCTCGGCTTATCAGAGAAGCCCAACATACACATGACATGAA	861
DB	781	TCATAACTACTTAACTCTCGGCTTATCAGAGAAGCCCAACATACACATGACATGAA	840
QY	862	GTAGCAGAGTGTTCACAAAAATTAATCTCAAGAGGAGCCCAACATATGAGGAGTCCC	921
DB	841	GTAGCAGAGTGTTCACAAAAATTAATCTCAAGAGGAGCCCAACATATGAGGAGTCCC	900
QY	922	AATAAGCCCAACAGCTGGACTGAGAAATCAGGCTGGAAAAATACCAGAGAAAGTACTCCA	981
DB	901	AATAAGCCCAACAGCTGGACTGAGAAATCAGGCTGGAAAAATACCAGAGAAAGTACTCCA	960
QY	982	ATGCGACGAATTCAGATGGTCTTGTCTAAGGGAGAAACGATGAACAGTATCTAACACA	1041
DB	961	ATGCGACGAATTCAGATGGTCTTGTCTAAGGGAGAAACGATGAACAGTATCTAACACA	1020
QY	1042	TTAACTTTCACAAATGGCTTGGAAAGGAGAACTAAAAACCTTACAGTGAAGACACTTTAGG	1101
DB	1021	TTAACTTTCACAAATGGCTTGGAAAGGAGAACTAAAAACCTTACAGTGAAGACACTTTAGG	1080
QY	1102	GACTTCCAATATTTCCCAATTTCTATGGCTACTGAAAGTATTTGATTCAGAAAAAGAA	1161
DB	1081	GACTTCCAATATTTCCCAATTTCTATGGCTACTGAAAGTATTTGATTCAGAAAAAGAA	1140
QY	1162	GCAAAAGAGAAAGAAACACTGATTACTATCATGAAAGCACTGATTCACATTTGTAAGATG	1221
DB	1141	GCAAAAGAGAAAGAAACACTGATTACTATCATGAAAGCACTGATTCACATTTGTAAGATG	1200
QY	1222	ATGGTGAATATGGAACAATATCTCAGAGAAAGTGTTCCTTACCTTGAAGAACTTTGAT	1281
DB	1201	ATGGTGAATATGGAACAATATCTCAGAGAAAGTGTTCCTTACCTTGAAGAACTTTGAT	1260
QY	1282	GAAATGATTTGCTTTCAGACCAAAACAGCTAGAAAAAATGCTACTGACATATTAAGC	1341
DB	1261	GAAATGATTTGCTTTCAGACCAAAACAGCTAGAAAAAATGCTACTGACATATTAAGC	1320
QY	1342	AAGCTTTTCCAGCACCATCAGAGAGAGTCTATGAAGAAACAGACAGTACCAAGGAAGAA	1401
DB	1321	AAGCTTTTCCAGCACCATCAGAGAGAGTCTATGAAGAAACAGACAGTACCAAGGAAGAA	1380
QY	1402	GCAGCTAAGATGGAAGAAAGTATGGAAGCTTGAAGGATTCACAAAAAGATGATTAATCC	1461
DB	1381	GCAGCTAAGATGGAAGAAAGTATGGAAGCTTGAAGGATTCACAAAAAGATGATTAATCC	1440
QY	1462	AACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAGCCCTATTGGAAGCCATC	1521
DB	1441	AACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAGCCCTATTGGAAGCCATC	1500
QY	1522	AGAAAAATATTGAAATGTTGAAGAAACATGACAAAAAGGGGAAATTAAGAGATTTATGAC	1581
DB	1501	AGAAAAATATTGAAATGTTGAAGAAACATGACAAAAAGGGGAAATTAAGAGATTTATGAC	1560
QY	1582	CTTTCAAGATGAGAGACTTCATCAATAAAGCTGATGCTTATGTTGGAGAAAGGCATC	1641
DB	1561	CTTTCAAGATGAGAGACTTCATCAATAAAGCTGATGCTTATGTTGGAGAAAGGCATC	1620
QY	1642	CTTTCAAGAGGAAAGCCGAGGCCATCAAGCCATTTATAGCAGCTCTGTAAAAATGGCAA	1701
DB	1621	CTTTCAAGAGGAAAGCCGAGGCCATCAAGCCATTTATAGCAGCTCTGTAAAAATGGCAA	1680
QY	1702	AAGATCCAGGAGCTCTTCACTGTTTTCAGAAAAACATAATATAGCTTAAACACTTTCTAT	1761
DB	1681	AAGATCCAGGAGCTCTTCACTGTTTTCAGAAAAACATAATATAGCTTAAACACTTTCTAT	1740
QY	1762	TCTGTGATTAATAATTTTGTGACCCCAAGGTTATTAGAAGTCTCAATTTACAGTAGTTA	1821

Db 1741 TCTGTGATTAATAATTTTGGACCCAGGGTTATTAGAAAGTGGCTGAATTTACAGTAGTTA 1800

QY 1822 ACCTTTTACAAGTGGTTAAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT 1881

Db 1801 ACCTTTACAAGTGGTTAAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT 1860

QY 1882 TGTATGTAAGCTGAGA 1897

Db 1861 TGTATGTAAGCTGAAA 1876

RESULT 8

US-10-140-471-89

; Sequence 89, Application US/10140471

; Publication No. US2003013887A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330RIC163

; CURRENT APPLICATION NUMBER: US/10/140.471

; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 89

; LENGTH: 1893

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-140-471-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 GTCTCCGGGTACAGGAACTTCAGCACCCAGGGCGGACAGCGCTCCCTCTACCTGGA 81

Db 1 GTCTCCGGGTACAGGAACTTCAGCACCCAGGGCGGACAGCGCTCCCTCTACCTGGA 60

QY 82 GACTTGACTCCCGCGCGCCCAACCCCTGCTTATCCCTTGACCGTGCAGTGTGAGATCC 141

Db 61 GACTTGACTCCCGCGCGCCCAACCCCTGCTTATCCCTTGACCGTGCAGATCC 120

QY 142 TGCAGCCGCCAGTCCCGGCCCTCTCCCGCCCAACCCCTGCTTCCCTGCTTCCCTGT 201

Db 121 TGCAGCCGCCAGTCCCGGCCCTCTCCCGCCCAACCCCTGCTTCCCTGCTTCCCTGT 180

QY 202 TTTTACTCTCTCTTTTCAATTAACAAAAGCTACAGCTCCAGGAGCCAGCGCGGGCT 261

Db 181 TTTTACTCTCTCTTTTCAATTAACAAAAGCTACAGCTCCAGGAGCCAGCGCGGGCT 240

QY 262 GTGACCCCAAGCCGAGCGGTGGAAGTATGGGTTCCTCGGACCCGCGACTTGGATTTGGTG 321

Db 241 GTGACCCCAAGCCGAGCGGTGGAAGTATGGGTTCCTCGGACCCGCGACTTGGATTTGGTG 300

QY 322 TTAGTGCTCCCGATTCAAGCTTTCCCAAACTGGAGAACCGAAGCAAAATCTCTACAT 381

Db 301 TTAGTGCTCCCGATTCAAGCTTTCCCAAACTGGAGAACCGAAGCAAAATCTCTACAT 360

QY 382 AATAGAGAAATTAAGTGCAGAAAGACCTTTGAAATGAACAGATGCTGAAAGCAGAAGAC 441

Db 361 AATAGAGAAATTAAGTGCAGAAAGACCTTTGAAATGAACAGATGCTGAAAGCAGAAGAC 420

QY 442 AAGATTAATAAAACATATCTCCAGAAACAGCCAGGTGAGAGCAACTATCTTTTGT 501

Db 421 AAGATTAATAAAACATATCTCCAGAAACAGCCAGGTGAGAGCAACTATCTTTTGT 480

QY 502 GATAACTTTGAACCTGCTAAGGGCAATAACAGAAAAAGAAAAATTTGAGAAACAGAA 561

Db 481 GATAACTTTGAACCTGCTAAGGGCAATAACAGAAAAAGAAAAATTTGAGAAACAGAA 540

QY 562 TCTATAGAAGCTCCCACTTTGATATAAGTTGGAAGATGTTGATTAACCAAG 621

Db 541 TCTATAGAAGCTCCCACTTTGATATAAGTTGGAAGATGTTGATTAACCAAG 600

QY 622 AATCGAAAACCTGATCGATGATGATGATGATGATGATGATGATGATGATGATGAT 581

Db 601 AATCGAAAACCTGATCGATGATGATGATGATGATGATGATGATGATGATGATGAT 660

QY 682 GATGATCCAGATGCTTTCATCACTAGACGGGACTTCTTTAAACCGCTGAACACATGTC 741

Db 661 GATGATCCAGATGCTTTCATCACTAGACGGGACTTCTTTAAACCGCTGAACACATGTC 720

QY 742 CATAAATCGCTGCCAGGATTTATGAAGAAATATGACAGCGCGTGTGACAAAGATGTT 801

Db 721 CATAAATCGCTGCCAGGATTTATGAAGAAATATGACAGCGCGTGTGACAAAGATGTT 780

QY 802 TCTAAACTACTTAATCTCGGCTTTATCAGAGAACCAAGCAGACATACACTGGAAGATGA 861

Db 781 TCTAAACTACTTAATCTCGGCTTTATCAGAGAACCAAGCAGACATACACTGGAAGATGA 840

QY 862 GTAGCAGAGGTTTACAAAAATTAATCTCAAGAGGAGCCAACTATATGAGGAGGATCC 921

Db 841 GTAGCAGAGGTTTACAAAAATTAATCTCAAGAGGAGCCAACTATATGAGGAGGATCC 900

QY 922 AATAAGCCCAACAGCTGGACTGAGATCAGGCTGGAATAATACAGAGAAAGTACTCA 981

Db 901 AATAAGCCCAACAGCTGGACTGAGATCAGGCTGGAATAATACAGAGAAAGTACTCA 960

QY 982 ATGGCAGCAATTCAGAGATGGTCTTCTAAGGGAGAAACAGATGAAACAGTATCTAACACA 1041

Db 961 ATGGCAGCAATTCAGAGATGGTCTTCTAAGGGAGAAACAGATGAAACAGTATCTAACACA 1020

QY 1042 TTAACCTTGACAAATGGCTTGAAGAGGAGAACTAAACCTACAGTCAAGACACTTTAGG 1101

Db 1021 TTAACCTTGACAAATGGCTTGAAGAGGAGAACTAAACCTACAGTCAAGACACTTTAGG 1080

QY 1102 GACTTCCCAATATTTCCCAAAATTTCTATCGCTTACTGAAAGATTTGATTCAGAAAAAGAA 1161

Db 1081 GACTTCCCAATATTTCCCAAAATTTCTATCGCTTACTGAAAGATTTGATTCAGAAAAAGAA 1140

QY 1162 GCAAAAGAGAAAGAAACACTGATTTACTATCATGATGAAACACTGATTTGCTGAGATG 1221

Db 1141 GCAAAAGAGAAAGAAACACTGATTTACTATCATGATGAAACACTGATTTGCTGAGATG 1200

QY 1222 ATGTGTAATATGGAACAATATCTCCAGAGAGGCTTTCCCTACCTTGAAACTTTGGAT 1281

Db 1201 ATGTGTAATATGGAACAATATCTCCAGAGAGGCTTTCCCTACCTTGAAACTTTGGAT 1260

QY 1282 GAAATGATGCTTCTTCAGACCAAAAACAGCTAGAAAAAATGCTACTGACATATTAAGC 1341

Db 1261 GAAATGATGCTTCTTCAGACCAAAAACAGCTAGAAAAAATGCTACTGACATATTAAGC 1320

QY 1342 AAGCTTTTCCAGCACCATCAGAGAAAGTATGAAAGAAACAGACAGTACCAAGAGAA 1401

Db 1321 AAGCTTTTCCAGCACCATCAGAGAAAGTATGAAAGAAACAGACAGTACCAAGAGAA 1380

QY 1402 GCAGCTAAGATGGAAGAAAGATATGGAAGCTTGAAGGATTCACAAAAAGATGATACTCC 1461

Db 1381 GCAGCTAAGATGGAAGAAAGATATGGAAGCTTGAAGGATTCACAAAAAGATGATACTCC 1440

QY 1462 AACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAAGCTATTGGAAAGCCATC 1521  
 Db 1441 AACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAAGCTATTGGAAAGCCATC 1500  
 QY 1522 AGAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGAAATAAAGAAATATGAC 1581  
 Db 1501 AGAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGAAATAAAGAAATATGAC 1560  
 QY 1582 CTTTCAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTTGGAAGAGGCATC 1641  
 Db 1561 CTTTCAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTTGGAAGAGGCATC 1620  
 QY 1642 CTTGACAAAGGAAAGCCGAGGCGCATCAAGCGCATTTATAGCAGCCTGTAAAAATGCAA 1701  
 Db 1621 CTTGACAAAGGAAAGCCGAGGCGCATCAAGCGCATTTATAGCAGCCTGTAAAAATGCAA 1680  
 QY 1702 AAGATCCAGAGTCTTCAACTGTTTCAGAAACATATATAGCTTAAACACATCTTAAT 1761  
 Db 1681 AAGATCCAGAGTCTTCAACTGTTTCAGAAACATATATAGCTTAAACACATCTTAAT 1740  
 QY 1762 TCTGTGATTAAATTTTTCAGCCCAAGGGTTATTAGAAAGTCTGTAATTTACAGTAGTTA 1821  
 Db 1741 TCTGTGATTAAATTTTTCAGCCCAAGGGTTATTAGAAAGTCTGTAATTTACAGTAGTTA 1800  
 QY 1822 ACCTTTTACAAAGTGGTTAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT 1881  
 Db 1801 ACCTTTTACAAAGTGGTTAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT 1860  
 QY 1882 TGTATGTAAGCTGAGA 1897  
 Db 1861 TGTATGTAAGCTGAAA 1876

RESULT 9

US-10-140-807-89  
 : Sequence 89, Application US/10140807  
 : Publication No. US20030134354A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Baker, Kevin P.  
 : APPLICANT: Beresini, Maureen  
 : APPLICANT: DeForge, Laura  
 : APPLICANT: Desnoyers, Luc  
 : APPLICANT: Filvaroff, Ellen  
 : APPLICANT: Gao, Wei-Qiang  
 : APPLICANT: Gerritsen, Mary E.  
 : APPLICANT: Goddard, Audrey  
 : APPLICANT: Godowski, Paul J.  
 : APPLICANT: Gurney, Austin L.  
 : APPLICANT: Sherwood, Steven  
 : APPLICANT: Smith, Victoria  
 : APPLICANT: Stewart, Timothy A.  
 : APPLICANT: Tumas, Daniel  
 : APPLICANT: Watanabe, Colin K  
 : APPLICANT: Wood, William  
 : APPLICANT: Zhang, Zemin  
 : TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 : FILE REFERENCE: P3330RIC174  
 : CURRENT APPLICATION NUMBER: US/10/140,807  
 : Prior Application removed - See File Wrapper or Palm  
 : NUMBER OF SEQ ID NOS: 550  
 : SEQ ID NO 89  
 : LENGTH: 1893  
 : TYPE: DNA  
 : ORGANISM: Homo Sapien  
 US-10-140-807-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 22 GTCTCCGCGTCACAGAACTTCAGCACCCAGGCGGACAGCGCTCCCTCTACCTGGA 81

Db 1 GTCTCCGCGTCACAGAACTTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGA 60  
 QY 82 GACTTGACTCCCGCGGCCCCCAACCCCTGCTTATCCCTTGACCGTTCGAGTGTGACAGATCC 141  
 Db 61 GACTTGACTCCCGCGGCCCCCAACCCCTGCTTATCCCTTGACCGTTCGAGTGTGACAGATCC 120  
 QY 142 TGACAGCGCCAGTCCCGGCCCTCTCCCGCCCAACCCCTGCTTATCCCTTGCTGCTCTTCTGT 201  
 Db 121 TGACAGCGCCAGTCCCGGCCCTCTCCCGCCCAACCCCTGCTTATCCCTTGCTGCTCTTCTGT 180  
 QY 202 TTTTACT 261  
 Db 181 TTTTACT 240  
 QY 262 GTACCCCAAGCCGAGCGTGAAGAATGGGGTCTCTCGGGACCGGCACTTTGGATTCTGGTG 321  
 Db 241 GTACCCCAAGCCGAGCGTGAAGAATGGGGTCTCTCGGGACCGGCACTTTGGATTCTGGTG 300  
 QY 322 TTAGTCTCTCCGATTCAGCTTTCCCAACCTGGAGGAGCCCAAGCAATCTCTACAT 381  
 Db 301 TTAGTCTCTCCGATTCAGCTTTCCCAACCTGGAGGAGCCCAAGCAATCTCTACAT 360  
 QY 382 AATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAAGAC 441  
 Db 361 AATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAAGAC 420  
 QY 442 AAGATTAAAAAACAATATCTCCAGAAAAACAGCCAGGTCAGAGCAACTATTCTTTTGT 501  
 Db 421 AAGATTAAAAAACAATATCTCCAGAAAAACAGCCAGGTCAGAGCAACTATTCTTTTGT 480  
 QY 502 GATACTTCAACTGCTTAAGGGCAATACAGAAAAAGGAAAAAATTCAGAAAAAGACAA 561  
 Db 481 GATACTTCAACTGCTTAAGGGCAATACAGAAAAAGGAAAAAATTCAGAAAAAGACAA 540  
 QY 562 TCTATAAGAAAGCTCCCACTTTGATATAAGTTGAATGTGAAGATGTTGATTCAACCAAG 621  
 Db 541 TCTATAAGAAAGCTCCCACTTTGATATAAGTTGAATGTGAAGATGTTGATTCAACCAAG 600  
 QY 622 AATCGAAAACTGATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATTAATTTCAA 681  
 Db 601 AATCGAAAACTGATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATTAATTTCAA 660  
 QY 682 GATGATCCAGATGGTCTTCATCAACTAGACGGGACTCTTTAAACCGCTGAACACATTTGC 741  
 Db 661 GATGATCCAGATGGTCTTCATCAACTAGACGGGACTCTTTAAACCGCTGAACACATTTGC 720  
 QY 742 CATATAAATCGCTGCCAGGATTTATGAAGAAATGACAGAGCGCTGTTTGACAAAGATTGT 801  
 Db 721 CATATAAATCGCTGCCAGGATTTATGAAGAAATGACAGAGCGCTGTTTGACAAAGATTGT 780  
 QY 802 TCTAAACTACTTTAATCTCGGCTTATACAGAAAAAGCAAGCAATACACTGGAAGATGAA 861  
 Db 781 TCTAAACTACTTTAATCTCGGCTTATACAGAAAAAGCAAGCAATACACTGGAAGATGAA 840  
 QY 862 GTAGCAGAGGTTTTACAAAAATTAATCTCAAGGAAAGCAACAATTTATGAGGAGGATCCC 921  
 Db 841 GTAGCAGAGGTTTTACAAAAATTAATCTCAAGGAAAGCAACAATTTATGAGGAGGATCCC 900  
 QY 922 AATAGCCCAAGCTGAGATGAGATCAGGCTGGAAAAATACCAAGAGAAAGTACTCCA 981  
 Db 901 AATAGCCCAAGCTGAGATGAGATCAGGCTGGAAAAATACCAAGAGAAAGTACTCCA 960  
 QY 982 ATGGCAGCAATTCAGATGGTCTTCTAAGGAGAAAAACGATGAACAGATATCTAACACA 1041  
 Db 961 ATGGCAGCAATTCAGATGGTCTTCTAAGGAGAAAAACGATGAACAGATATCTAACACA 1020  
 QY 1042 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTAAAACTACAGTGAAGACAACTTTAGG 1101  
 Db 1021 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTAAAACTACAGTGAAGACAACTTTAGG 1080  
 QY 1102 GACTTCCAAATATTTCCCAAAATTTCTATGCGGCTACTGAAAATGATTGATTCAGAAAAAGAA 1161

Db 1081 GAATCCCAATATTTCCCAATTTCTATCGCTACTGAAAGATTTGATTCAGAAAAAGAA 1140  
QY 1162 GCAAAAGAGAAGAAACACTGATTACTATCATGATGAAACACACTGATTGACTTTGTGAAGATG 1221  
Db 1141 CCAAAGAGAAGAAACACTGATTACTATCATGATGAAACACACTGATTGACTTTGTGAAGATG 1200  
QY 1222 ATGTGAAATATGAAACAATATCTCCAGAAAGGTGTTCTTACCTTTGAAAACCTTGGAT 1281  
Db 1201 ATGTGAAATATGAAACAATATCTCCAGAAAGGTGTTCTTACCTTTGAAAACCTTGGAT 1260  
QY 1282 GAATGATGCTCTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGACAAATATAGC 1341  
Db 1261 GAAATGATGCTCTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGACAAATATAGC 1320  
QY 1342 AAGCTTTTCCAGACCATCAGAGAAGTCTATGAAGAAACAGACAGTACCACGAAGAGAA 1401  
Db 1321 AAGCTTTTCCAGACCATCAGAGAAGTCTATGAAGAAACAGACAGTACCACGAAGAGAA 1380  
QY 1402 GCAGCTAAGATGGAAGGAATATGGAAGCTTGAAGATTCCACAAAAGATGATAACTCC 1461  
Db 1381 GCAGCTAAGATGGAAGGAATATGGAAGCTTGAAGATTCCACAAAAGATGATAACTCC 1440  
QY 1462 AACCAGGAGAAAGACAGATGACCCAAAGGAAACAGAGGCTATTTGGAAGCCATC 1521  
Db 1441 AACCAGGAGAAAGACAGATGACCCAAAGGAAACAGAGGCTATTTGGAAGCCATC 1500  
QY 1522 AGAAAAATATTTGAATGCTTGAAGAAACATCACAAAAGGGAATTAAGAAGATTATGAC 1581  
Db 1501 AGAAAAATATTTGAATGCTTGAAGAAACATCACAAAAGGGAATTAAGAAGATTATGAC 1560  
QY 1582 CTTTCAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATC 1641  
Db 1561 CTTTCAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATC 1620  
QY 1642 CTTGACAGGAAGAGCGAGCCCATCAAGCGCATTTATACAGCGCTGTAATAATGGCAA 1701  
Db 1621 CTTGACAGGAAGAGCGAGCCCATCAAGCGCATTTATACAGCGCTGTAATAATGGCAA 1680  
QY 1702 AAGATCCAGGAGTCTTTCACTGTTTCAGAAAACATATATAGCTTAAACACACTTCTAAT 1761  
Db 1681 AAGATCCAGGAGTCTTTCACTGTTTCAGAAAACATATATAGCTTAAACACACTTCTAAT 1740  
QY 1762 TCTGTGATATAAATTTTGTACCAAGGGTTATTAGAAAGTCTCAATTTACAGTAGTTA 1821  
Db 1741 TCTGTGATATAAATTTTGTACCAAGGGTTATTAGAAAGTCTCAATTTACAGTAGTTA 1800  
QY 1822 ACCTTTTACAGTGGTTAAACATAGCTTTCTTCCCGTAAAAACATATCTGAAAGTAAAGT 1881  
Db 1801 ACCTTTTACAGTGGTTAAACATAGCTTTCTTCCCGTAAAAACATATCTGAAAGTAAAGT 1860  
QY 1882 TGTATGTAAGCTGAGA 1897  
Db 1861 TGTATGTAAGCTGAAA 1876

RESULT 10

US-10-140-922-89  
; Sequence 89, Application US/10140922

; Publication No. US20030138889A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Collin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C179  
; CURRENT APPLICATION NUMBER: US/10/140,922  
; CURRENT FILING DATE: 2002-05-07  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 89  
; LENGTH: 1893  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-140-922-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGCGGACAGCGCTCCCTCTACTCGA 81  
Db 1 GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGCGGACAGCGCTCCCTCTACTCGA 60  
QY 82 GACTTGACTCCCGCGCGCCCAACCTGCTTATCCCTTGACCGTGCAGTGTCCAGAGATCC 141  
Db 61 GACTTGACTCCCGCGCGCCCAACCTGCTTATCCCTTGACCGTGCAGTGTCCAGAGATCC 120  
QY 142 TGCAGCCGCCAGTCCCGCGCCCTCTCCCGCCCAACACCCACCTCTGCTGCTTCTGT 201  
Db 121 TGCAGCCGCCAGTCCCGCGCCCTCTCCCGCCCAACACCCACCTCTGCTGCTTCTGT 180  
QY 202 TTTTACTCTCTTTTCATTATACAAAAGCTACAGCTCCAGGAGCCAGCGCGGCT 261  
Db 181 TTTTACTCTCTTTTCATTATACAAAAGCTACAGCTCCAGGAGCCAGCGCGGCT 240  
QY 262 GTGACCCAAAGCGGAGCGTGGGAAGATGGGTTCCTCGGACCGGACCTTGGATTCTGGTG 321  
Db 241 GTGACCCAAAGCGGAGCGTGGGAAGATGGGTTCCTCGGACCGGACCTTGGATTCTGGTG 300  
QY 322 TTAGTGCTCCGATTCAGCTTTCCCAACCTTGAGGAAGCAAAATCTCTACAT 381  
Db 301 TTAGTGCTCCGATTCAGCTTTCCCAACCTTGAGGAAGCAAAATCTCTACAT 360  
QY 382 AATAGAGAAATTAAGTGCAGAAAGACCTTTTGAATGAACAGATTGCTGGAAGCAAGAAC 441  
Db 361 AATAGAGAAATTAAGTGCAGAAAGACCTTTTGAATGAACAGATTGCTGGAAGCAAGAAC 420  
QY 442 AAGATTAAAAAACATATCTCCAGAAAACAGCCAGGTCAGAGCAACTATTCTTTTGT 501  
Db 421 AAGATTAAAAAACATATCTCCAGAAAACAGCCAGGTCAGAGCAACTATTCTTTTGT 480  
QY 502 GATACTTTGAACCTGCTAAGGCAATAACAGAAAAGGAAAAAATTTGAGAAAGAACAA 561  
Db 481 GATACTTTGAACCTGCTAAGGCAATAACAGAAAAGGAAAAAATTTGAGAAAGAACAA 540  
QY 562 TCTATAAGAACTCCCACTTGAATAAGTTGAATGTGAAGATGTTGATTCAACCAAG 621  
Db 541 TCTATAAGAACTCCCACTTGAATAAGTTGAATGTGAAGATGTTGATTCAACCAAG 600  
QY 622 AATCGAAAACCTGATCGATTATGACTCTACTAAGAGTGGATTGGATCATATAATTTCAA 681  
Db 601 AATCGAAAACCTGATCGATTATGACTCTACTAAGAGTGGATTGGATCATATAATTTCAA 660  
QY 682 GATGATCCAGATGCTTTTCATCAACTAGACGGGACTCTCTTTAACCGCTGAAGACATGTC 741  
Db 661 GATGATCCAGATGCTTTTCATCAACTAGACGGGACTCTCTTTAACCGCTGAAGACATGTC 720  
QY 742 CATAAAATCGCTGCCAGGATTATGAAGAAATGACAGAGCGCTGTTTGACAGAGATTGTT 801  
Db 721 CATAAAATCGCTGCCAGGATTATGAAGAAATGACAGAGCGCTGTTTGACAGAGATTGTT 780

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QY 802 TCTAACTACTTAATCTCGGCTTATCACAGAAAGCCAAAGCACATACACTGGAAGATGAA 861
Db 781 TCTAACTACTTAATCTCGGCTTATCACAGAAAGCCAAAGCACATACACTGGAAGATGAA 840
QY 862 GTACGAGAGGTTTACAAAATTAATCTCAAGAGAGCCACAAATTAATGAGGAGATCCC 921
Db 841 GTACGAGAGGTTTACAAAATTAATCTCAAGAGAGCCACAAATTAATGAGGAGATCCC 900
QY 922 AATAAGCCCAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAGTGACTCCA 981
Db 901 AATAAGCCCAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAGTGACTCCA 960
QY 982 ATGCGACAAATTCAGATGGCTTCTGAAGAGGAGAAACGATGAACAGTATCTAACACA 1041
Db 961 ATGCGACAAATTCAGATGGCTTCTGAAGAGGAGAAACGATGAACAGTATCTAACACA 1020
QY 1042 TTAACCTTGCAAAATGCTTGGAAAGGAGAACTAAAACCTACAGTGAAAGCAACTTTAGG 1101
Db 1021 TTAACCTTGCAAAATGCTTGGAAAGGAGAACTAAAACCTACAGTGAAAGCAACTTTAGG 1080
QY 1102 GACTTCCAAATTTCCCAAAATTTCTATGCGCTACTGAAAAAGTATTGATTGAAAAAGAA 1161
Db 1081 GACTTCCAAATTTCCCAAAATTTCTATGCGCTACTGAAAAAGTATTGATTGAAAAAGAA 1140
QY 1162 GCRAAGAGAGAAAGAACACTGATTACTATCATGAACACACTGATTGACTTTGTGAAGATG 1221
Db 1141 GCRAAGAGAGAAAGAACACTGATTACTATCATGAACACACTGATTGACTTTGTGAAGATG 1200
QY 1222 ATGCTGAATATGAAACAATATCTCCAGAGAGAGGTGTTTCCCTACCTTGAAGAACTGGAT 1281
Db 1201 ATGCTGAATATGAAACAATATCTCCAGAGAGAGGTGTTTCCCTACCTTGAAGAACTGGAT 1260
QY 1282 GAAATGATGCTTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGACAAATATAAGC 1341
Db 1261 GAAATGATGCTTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGACAAATATAAGC 1320
QY 1342 AAGCTTTTCCAGCACCATCAGAGAGAGATCATGAGAAACACAGACAGTACCAGAGAGAA 1401
Db 1321 AAGCTTTTCCAGCACCATCAGAGAGAGATCATGAGAAACACAGACAGTACCAGAGAGAA 1380
QY 1402 GCAGCTAAGATGAAAGGAATATGGAAGCTTGAAGGATTCACAAAGATGATACTCC 1461
Db 1381 GCAGCTAAGATGAAAGGAATATGGAAGCTTGAAGGATTCACAAAGATGATACTCC 1440
QY 1462 AACCCAGGAGGAAGACAGATGAACCCAAAGGAAAAACAGAGCCCTATTGGAAGCCATC 1521
Db 1441 AACCCAGGAGGAAGACAGATGAACCCAAAGGAAAAACAGAGCCCTATTGGAAGCCATC 1500
QY 1522 AGAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAATTAAGAGATTTATGAC 1581
Db 1501 AGAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAATTAAGAGATTTATGAC 1560
QY 1582 CTTTCAAGATGAGAGACTTCATCAATAAACAGCTGATGCTTATGTGAGAGAAAGGCATC 1641
Db 1561 CTTTCAAGATGAGAGACTTCATCAATAAACAGCTGATGCTTATGTGAGAGAAAGGCATC 1620
QY 1642 CTTGACAGAGAGAACCCAGGCCATCAAGCGCATTTATAGAGCGCTGTAAAAATGGCAA 1701
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QY 1702 AAGATCCAGGAGTCTTTCAACTGTTTTCAGAAACATATATAGCTTAAACACTTCTAT 1761
Db 1681 AAGATCCAGGAGTCTTTCAACTGTTTTCAGAAACATATATAGCTTAAACACTTCTAT 1740
QY 1762 TCTGTGATTAATTTTTCAGCCCAAGGTTTATTAGAAAGTCTGAAATTTACAGTAGTTA 1821
Db 1741 TCTGTGATTAATTTTTCAGCCCAAGGTTTATTAGAAAGTCTGAAATTTACAGTAGTTA 1800
QY 1822 ACCTTTTCAAGTCTTAAACATAGCTTTCTCCGTTAAACATCTCTGAAAGTAAAGT 1881
Db 1801 ACCTTTTCAAGTCTTAAACATAGCTTTCTCCGTTAAACATCTCTGAAAGTAAAGT 1860
QY 1882 TGTATGTAAGCTGAGA 1897
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Db 1861 TGTATGTAAGCTGAAA 1876
RESULT 11
US-10-140-924-89
; Sequence 89, Application US/10140924
; Publication No. US20030134355A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Oiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: P330R1C177
; CURRENT APPLICATION NUMBER: US/10/140, 924
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 89
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-924-89
Query Match 92.5%; Score 1866.4; DB 12; Length 1893;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 22 GTCTCGCGCTCACAGGAACCTTCAGCACCCAGCGGCGGACAGCGCTCCCTCTTACCTGA 81
Db 1 GTCTCGCGCTCACAGGAACCTTCAGCACCCACAGCGGCGGACAGCGCTCCCTCTTACCTGA 60
QY 82 GACTTGACTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 141
Db 61 GACTTGACTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
QY 142 TCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 201
Db 121 TCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 202 TTTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 261
Db 181 TTTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 262 GTGACCCCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 321
Db 241 GTGACCCCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
QY 322 TTAGTGCTCCCGGATTTCAAGCTTTCCCAAACTGGAGGAAGCAAGCAAGCAAGCAAGCAAG 381
Db 301 TTAGTGCTCCCGGATTTCAAGCTTTCCCAAACTGGAGGAAGCAAGCAAGCAAGCAAGCAAG 360
QY 382 AATAGAGAAATTAAGTGCAGAAAGACTTTTGAATGAACAGATTTGCTGAAGCAAGCAAGCAAG 441
Db 361 AATAGAGAAATTAAGTGCAGAAAGACTTTTGAATGAACAGATTTGCTGAAGCAAGCAAGCAAG 420
QY 442 AAGATTAAAAAACAATATCTCCAGAAACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 501
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Db 421 AAGATTAAAAAACAATATCTCCAGAAAAAAGCCAGGTCAGAGCAACTATTTCTTTGTT 480  
QY 502 GATRACTTTGACCTGCTTAAGGCGCATACAGAAAGGAAAAATTTGAGAAAGAGACAA 561  
Db 481 GATACTTTGACCTGCTTAAGGCGCATACAGAAAGGAAAAATTTGAGAAAGAGACAA 540  
QY 562 TCTATAAGAAAGTCCCACTTTGATAAATGATTTGGAAGATGTTGATTCAACCAAG 621  
Db 541 TCTATAAGAAAGTCCCACTTTGATAAATGATTTGGAAGATGTTGATTCAACCAAG 600  
QY 622 AATCGAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 681  
Db 601 AATCGAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
QY 682 GATGATCCAGATGCTTCACTCACTAGACGGGACTCCTTTAAGCGCTGAAGACATGTC 741  
Db 661 GATGATCCAGATGCTTCACTCACTAGACGGGACTCCTTTAAGCGCTGAAGACATGTC 720  
QY 742 CATAAATCGCTGCCAGGATTTATGAAGAAATGACAGAGCGGTGTTTGACAAAGATTGTT 801  
Db 721 CATAAATCGCTGCCAGGATTTATGAAGAAATGACAGAGCGGTGTTTGACAAAGATTGTT 780  
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Db 781 TCTAACTACTTAATCTCGGCTTTATACAGAAAGCAAGCACATACACTGGAAGATGAA 840  
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Db 841 GTAGCAGAGGTTTACAAAAATTAATCTCAAGGAAGCCAAATATGAGGAGGATCCC 900  
QY 922 AATAAGCCACAAAGTGGACTGAGAAATCAGGCTGGAAAAATACCAGAGAAAGTGACTCCA 981  
Db 901 AATAAGCCACAAAGTGGACTGAGAAATCAGGCTGGAAAAATACCAGAGAAAGTGACTCCA 960  
QY 982 ATGGCAGCAATTCAGATGGCTTCTGCTAAGGAGAAACGATGAACAGTATCTAACACA 1041  
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QY 1162 GCAAAGAGAGAAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1221  
Db 1141 GCAAAGAGAGAAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200  
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QY 1282 GAAATGATGCTTTTCAGACCAAAACAAAGCTAGAAAAAATGCTTACTGACAATATAAGC 1341  
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QY 1342 AAGCTTTTCCAGCAACATCAGAGAAAGTCTATGAAGAAACAGACAGTACCAAGGAAGA 1401  
Db 1321 AAGCTTTTCCAGCAACATCAGAGAAAGTCTATGAAGAAACAGACAGTACCAAGGAAGA 1380  
QY 1402 CGAGCTAAGTGAAGAAAGATATGGAAGCTTGAAGGATTCACAAAAGATGATACTCC 1461  
Db 1381 CGAGCTAAGTGAAGAAAGATATGGAAGCTTGAAGGATTCACAAAAGATGATACTCC 1440  
QY 1462 AACCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAGCCCTATTTTGGAAGCCATC 1521  
Db 1441 AACCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAGCCCTATTTTGGAAGCCATC 1500  
QY 1522 AGAAAAAATATTGAATGTTGAAGAAACATGACAAAAAGGGGAAATTAAGAGATATGAC 1581  
Db 1501 AGAAAAAATATTGAATGTTGAAGAAACATGACAAAAAGGGGAAATTAAGAGATATGAC 1560

QY 1582 CTTTCAAGATGAGAGACTTCATCAATATAAACAAGCTGATGCTTATGTGGAGAAAGGCATC 1641  
Db 1561 CTTTCAAGATGAGAGACTTCATCAATATAAACAAGCTGATGCTTATGTGGAGAAAGGCATC 1620  
QY 1642 CTTGACAAAGGAGAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAATGGCAA 1701  
Db 1621 CTTGACAAAGGAGAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAATGGCAA 1680  
QY 1702 AAGATCCAGAGAGTCTTTCAACTGTTTCAGAAAAACATAATATAGCTTAAAAACACTTCTAAT 1761  
Db 1681 AAGATCCAGAGAGTCTTTCAACTGTTTCAGAAAAACATAATATAGCTTAAAAACACTTCTAAT 1740  
QY 1762 TCTGTGATTAAAAATTTTTTGACCCCAAGGGTTATTAGAAAAGTCTCAATTTACAGTAGTTA 1821  
Db 1741 TCTGTGATTAAAAATTTTTTGACCCCAAGGGTTATTAGAAAAGTCTCAATTTACAGTAGTTA 1800  
QY 1822 ACCTTTTACAAGTGGTTAAAAACATAGCTTTCTTCCCGTAAAAACATATCTGAAAGTAAAGT 1881  
Db 1801 ACCTTTTACAAGTGGTTAAAAACATAGCTTTCTTCCCGTAAAAACATATCTGAAAGTAAAGT 1860  
QY 1882 TGTATGTAAGCTGAGA 1897  
Db 1861 TGTATGTAAGCTGAAA 1876

RESULT 12  
US-10-140-926-89  
; Sequence 89, Application US/10140926  
; Publication No. US20030134356A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P33301C187  
; CURRENT APPLICATION NUMBER: US/10/140,926  
; CURRENT FILING DATE: 2002-05-07  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 89  
; LENGTH: 1893  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-140-926-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 22 GTCTCCGGGTACAGAGAACTTCAGACCCACAGGCGGACAGCGTCCCTCTACCTGGA 81  
Db 1 GTCTCCGGGTACAGAGAACTTCAGACCCACAGGCGGACAGCGTCCCTCTACCTGGA 60  
QY 82 GACTTGACTCCCGCGGCCCAACCGTGTTCCTTACCGTGTGAGTGTGAGATGCC 141  
Db .61 GACTTGACTCCCGCGGCCCAACCGTGTTCCTTACCGTGTGAGTGTGAGATGCC 120



QY 142 TGCAGCCGCGCCAGTCCCGGGCCCTCTCCCGCCCCACACCCACCCCTCTCGCTCTTCCTGT 201  
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 QY 202 TTTTACTCCCTCTTTTTCATATCAACAAAGAGCTACAGCTCCAGAGCCGCGCGGGCT 261  
 Db 181 TTTTACTCCCTCTTTTTCATATCAACAAAGAGCTACAGCTCCAGAGCCGCGCGGGCT 240  
 QY 262 GTGACCCAAAGCCGAGCTGGAAGAAATGGGGTTCCTCGGGACCCGCGCTCTGATTTCTGGTG 321  
 Db 241 GTGACCCAAAGCCGAGCTGGAAGAAATGGGGTTCCTCGGGACCCGCGCTCTGATTTCTGGTG 300  
 QY 322 TTAGTGTCCCGATTCAGCTTTCCCAACCTGGAGGAAGCCCAAGCAAAATCTCTACAT 381  
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 Db 421 AAGATTAAAAAACAATATCTCCAGAAACAAGCCAGGTCAGAGCAACTATCTTTTGT 480  
 QY 502 GATAACTTGAACCTGCTTAAGGGCAATTAACAGAAAGAAAAATTTGAGAAAGAAAGACAA 561  
 Db 481 GATAACTTGAACCTGCTTAAGGGCAATTAACAGAAAGAAAAATTTGAGAAAGAAAGACAA 540  
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 Db 541 TCTATAGAAGCTCCCACTTGATTAATGAAGTTCGAATGGAAGATTTGATTTCAACCAAG 600  
 QY 622 AATCGAAACTGATCGATGATTATGACTCTACTTAAGAGTGGATTTGATTCATAAATTTCAA 681  
 Db 601 AATCGAAACTGATCGATGATTATGACTCTACTTAAGAGTGGATTTGATTCATAAATTTCAA 660  
 QY 682 GATGATCCAGATGGCTTTCATCACTAGAGGGGACTCCTTTAACCGCTGAAGACATGTG 741  
 Db 661 GATGATCCAGATGGCTTTCATCACTAGAGGGGACTCCTTTAACCGCTGAAGACATGTG 720  
 QY 742 CATAAATCGCTCCAGGATTTATGAAGAAATGACAGAGCCGCTGTTGACAGATTTGT 801  
 Db 721 CATAAATCGCTCCAGGATTTATGAAGAAATGACAGAGCCGCTGTTGACAGATTTGT 780  
 QY 802 TCTAAACTACTTAATCTCGGCTTATCAGAAAGCCAGCAATACACTGGAAGATGAA 861  
 Db 781 TCTAAACTACTTAATCTCGGCTTATCAGAAAGCCAGCAATACACTGGAAGATGAA 840  
 QY 862 GTAGCAGAGTCTTACAAAATTAATCTCAAGGAAGCCCAACAAATATGAGGAGATCCC 921  
 Db 841 GTAGCAGAGTCTTACAAAATTAATCTCAAGGAAGCCCAACAAATATGAGGAGATCCC 900  
 QY 922 AATAAGCCCAAGCTGGACTGAGATCAGGCTGGAATAATACAGAGAAAGTACTCCA 981  
 Db 901 AATAAGCCCAAGCTGGACTGAGATCAGGCTGGAATAATACAGAGAAAGTACTCCA 960  
 QY 982 ATGGCAGCAATTCAGATGGCTTGTGAAGGAGAAACGATGAACATATCTTAACACA 1041  
 Db 961 ATGGCAGCAATTCAGATGGCTTGTGAAGGAGAAACGATGAACATATCTTAACACA 1020  
 QY 1042 TTAACCTTGACAAATGGCTTGAAGGAGAACTTAAACCTTACAGTGAACAACTTTAGG 1101  
 Db 1021 TTAACCTTGACAAATGGCTTGAAGGAGAACTTAAACCTTACAGTGAACAACTTTAGG 1080  
 QY 1102 GACTTCCAATATTTCCCAATTTCTATCGGCTACTGAAAGTATTGATTCAGAAAAGAA 1161  
 Db 1081 GAATCCCAATATTTCCCAATTTCTATCGGCTACTGAAAGTATTGATTCAGAAAAGAA 1140  
 QY 1162 GCAAGAGCAAGAAACACTGATTACTATCATGAAGAAACACTGATTGCTTTGTGAAGATG 1221  
 Db 1141 GCAAGAGCAAGAAACACTGATTACTATCATGAAGAAACACTGATTGCTTTGTGAAGATG 1200  
 QY 1222 ATGGTGAATATGGAACAATATCTCCAGAAAGAGTGTTCCTACTCTTGAACAACTTGGAT 1281

Db 1201 ATGGTGAATATGGAACAATATCTCCAGAAAGAGTGTTCCTACTACCTTGAACACTTGGAT 1260  
 QY 1282 GAATGATTTGCTCTTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGACAAATATAGC 1341  
 Db 1261 GAATGATTTGCTCTTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGACAAATATAGC 1320  
 QY 1342 AAGCTTTTCCAGCACCACCATCAGAGAGAGTCAATGAAGAGATTTCCACAAAAGATGATACTCC 1401  
 Db 1321 AAGCTTTTCCAGCACCACCATCAGAGAGAGTCAATGAAGAGATTTCCACAAAAGATGATACTCC 1380  
 QY 1402 GCAGCTAAGATGGAAGAGATATGGAAGCTTGAAGGATTTCCACAAAAGATGATACTCC 1461  
 Db 1381 GCAGCTAAGATGGAAGAGATATGGAAGCTTGAAGGATTTCCACAAAAGATGATACTCC 1440  
 QY 1462 AACCCAGGAGGAAGACAGATGAACCCAAAGGAAAAACAGAGCCCTATTTGGAGGCCATC 1521  
 Db 1441 AACCCAGGAGGAAGACAGATGAACCCAAAGGAAAAACAGAGCCCTATTTGGAGGCCATC 1500  
 QY 1522 AGAAAAAATTTGAATGGTTGAAGAAACATGACAAAAAGGGAATTAAGAGATTTATGAC 1581  
 Db 1501 AGAAAAAATTTGAATGGTTGAAGAAACATGACAAAAAGGGAATTAAGAGATTTATGAC 1560  
 QY 1582 CTTTCAAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTTATGTGGAGAAAGGCATC 1641  
 Db 1561 CTTTCAAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTTATGTGGAGAAAGGCATC 1620  
 QY 1642 CTTGACAAAGGAAGCCGAGGCCATCAAGCGGATTTATAGAGCCCTGTAAAAATGGCAA 1701  
 Db 1621 CTTGACAAAGGAAGCCGAGGCCATCAAGCGGATTTATAGAGCCCTGTAAAAATGGCAA 1680  
 QY 1702 AAGATCCAGGAGTCTTCAACTGTTTCAGAAAAACATAATATAGCTTAAACACTTCTTAAT 1761  
 Db 1681 AAGATCCAGGAGTCTTCAACTGTTTCAGAAAAACATAATATAGCTTAAACACTTCTTAAT 1740  
 QY 1762 TCTGTGATTAATAATTTTGGACCAAGGGTATTAGAAAAGTGTGTAATTTACAGTAGTTA 1821  
 Db 1741 TCTGTGATTAATAATTTTGGACCAAGGGTATTAGAAAAGTGTGTAATTTACAGTAGTTA 1800  
 QY 1822 ACCTTTTACAAGTGGTTAAACATAGCTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT 1881  
 Db 1801 ACCTTTTACAAGTGGTTAAACATAGCTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT 1860  
 QY 1882 TGTATGTAAGCTGAGA 1897  
 Db 1861 TGTATGTAAGCTGAAA 1876

RESULT 13

US-10-141-698-89  
 ; Sequence 89, Application US/10141698  
 ; Publication No. US20030134357A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3330R1C206



; CURRENT APPLICATION NUMBER: US/10/141.698  
 ; CURRENT FILING DATE: 2002-05-08  
 ; Prior Application removed - See Palm or File Wrapper  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 89  
 ; LENGTH: 1893  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-141-698-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	22	GTCTCCGCGTCACAGAACTTCAGCACCCACAGCGCGACAGCGCTCCCTCTACCTGGA	81
Db	1	GTCTCCGCGTCACAGAACTTCAGCACCCACAGCGCGACAGCGCTCCCTCTACCTGGA	60
Qy	82	GACTTGACTCCGCGCGCCCAACCCCTGCTTATCCCTTGACCGCTCGAGTGTGAGATCC	141
Db	61	GACTTGACTCCGCGCGCCCAACCCCTGCTTATCCCTTGACCGCTCGAGTGTGAGATCC	120
Qy	142	TGCAGCGCGCGAGTCCCGGCGCCCTCTCCGCGCCACACCCCTCTCTGCTTCTCTGT	201
Db	121	TGCAGCGCGCGAGTCCCGGCGCCCTCTCTCCGCGCCACACCCCTCTCTGCTTCTCTGT	180
Qy	202	TTTTTACTCTCTCTTTTCAATACAAAGCTACAGCTCCAGGAGCCCGCGCGGCT	261
Db	181	TTTTTACTCTCTCTTTTCAATACAAAGCTACAGCTCCAGGAGCCCGCGCGGCT	240
Qy	262	GTGACCCCAAGCGCGAGTGGGAAGTGGGTTCTCGGACCGCGCTTGGAATCTCTGTG	321
Db	241	GTGACCCCAAGCGCGAGTGGGAAGTGGGTTCTCGGACCGCGCTTGGAATCTCTGTG	300
Qy	322	TTAGTGTCTCCGATTCAGCTTTCCCAAGCTTGAGAGCTGGAGAGCCAGCAATCTCTACAT	381
Db	301	TTAGTGTCTCCGATTCAGCTTTCCCAAGCTTGAGAGCTGGAGAGCCAGCAATCTCTACAT	360
Qy	382	AATAGAGAAATTAAGTCAGAGAAAGACCTTTGAATGAACAGATTTGCTGAAGCAGAGAAGAC	441
Db	361	AATAGAGAAATTAAGTCAGAGAAAGACCTTTGAATGAACAGATTTGCTGAAGCAGAGAAGAC	420
Qy	442	AAGATTAAAAAACAATATCTCCAGAAACAGCCAGGTTCAGAGCAACTATCTTTTGT	501
Db	421	AAGATTAAAAAACAATATCTCCAGAAACAGCCAGGTTCAGAGCAACTATCTTTTGT	480
Qy	502	GATAACTTGACCTGTCTAAGGCAATACAGAAAGAAAGAAATTTGAGAAAGAACAA	561
Db	481	GATAACTTGACCTGTCTAAGGCAATACAGAAAGAAAGAAATTTGAGAAAGAACAA	540
Qy	562	TCTATAAGAGCTCCCGCTTGATAAAGTTGAATGTGAAGATTTGATTCACCAAG	621
Db	541	TCTATAAGAGCTCCCGCTTGATAAAGTTGAATGTGAAGATTTGATTCACCAAG	600
Qy	622	AATCGAAACTGATCGATGATTAAGTCTACTAAGAGTGGATTTGATTCATAATTTCAA	681
Db	601	AATCGAAACTGATCGATGATTAAGTCTACTAAGAGTGGATTTGATTCATAATTTCAA	660
Qy	682	GATGATCCAGATGGTCTTCACTAAGAGCGGACTCCTTTAACCCTGAGACATTTGTC	741
Db	661	GATGATCCAGATGGTCTTCACTAAGAGCGGACTCCTTTAACCCTGAGACATTTGTC	720
Qy	742	CATATAATCGTCCGAGATTTATGAAGAAATGACAGAGCCGCTTTGACAGATTTGT	801
Db	721	CATATAATCGTCCGAGATTTATGAAGAAATGACAGAGCCGCTTTGACAGATTTGT	780
Qy	802	TCTAAACTACTTAATCTCGGCTTTATCACAGAAAGCCAGCAATACACTGGAGATGAA	861
Db	781	TCTAAACTACTTAATCTCGGCTTTATCACAGAAAGCCAGCAATACACTGGAGATGAA	840
Qy	862	GTAGCAGAGGTTTTTACAAAAATTAATCTCAAGAGAGCCCAACAAATTTATGAGGAGATCCC	921
Db	841	GTAGCAGAGGTTTTTACAAAAATTAATCTCAAGAGAGCCCAACAAATTTATGAGGAGATCCC	900

Qy	922	AATAAGCCCAAGCTGGACTGAGATCAGGCTGGAAAAATACAGAGAAAGTGA	981
Db	901	AATAAGCCCAAGCTGGACTGAGATCAGGCTGGAAAAATACAGAGAAAGTGA	960
Qy	982	ATGCGAGCAATTCAGATGCTTGTCTAAGGAGAAAAACGATGAACAGTATCTAAACACA	1041
Db	961	ATGCGAGCAATTCAGATGCTTGTCTAAGGAGAAAAACGATGAACAGTATCTAAACACA	1020
Qy	1042	TTAACCCTGCAAAATGCTTGGAAAGGAGAACTAAACCTACAGTGAAGCAACTTTAGG	1101
Db	1021	TTAACCCTGCAAAATGCTTGGAAAGGAGAACTAAACCTACAGTGAAGCAACTTTAGG	1080
Qy	1102	GACTTCCAATATTTCCCAAAATTTCTATGCGCTACTGAAAGCTATTGATTCAGAAAAAGAA	1161
Db	1081	GACTTCCAATATTTCCCAAAATTTCTATGCGCTACTGAAAGCTATTGATTCAGAAAAAGAA	1140
Qy	1162	GCAAAGAGAAAGAACACTGATTACTATCATGAAACACACTGATTTGTGAAGATG	1221
Db	1141	GCAAAGAGAAAGAACACTGATTACTATCATGAAACACACTGATTTGTGAAGATG	1200
Qy	1222	ATGCTGAATATGAAACAAATATCTCCAGAAAGGTGTTCTTACCTTGAACAACTTTGAT	1281
Db	1201	ATGCTGAATATGAAACAAATATCTCCAGAAAGGTGTTCTTACCTTGAACAACTTTGAT	1260
Qy	1282	GAAATGATTTGCTTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGACAAATATAAGC	1341
Db	1261	GAAATGATTTGCTTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGACAAATATAAGC	1320
Qy	1342	AAGCTTTTCCAGACCAATCATGAGAAAGTCTATGAAGAAACAGACAGTACCAAGGAAGAA	1401
Db	1321	AAGCTTTTCCAGACCAATCATGAGAAAGTCTATGAAGAAACAGACAGTACCAAGGAAGAA	1380
Qy	1402	GCAGCTAAGATGGAAGGAATATGGAAGCTTTGAAGCTTTCCACAAAAGATGATAACTCC	1461
Db	1381	GCAGCTAAGATGGAAGGAATATGGAAGCTTTGAAGCTTTCCACAAAAGATGATAACTCC	1440
Qy	1462	AACCCAGGAGAAAGACAGATGAACCCAAAGGAAAAACAGAGCTTATTTGGAAGCCATC	1521
Db	1441	AACCCAGGAGAAAGACAGATGAACCCAAAGGAAAAACAGAGCTTATTTGGAAGCCATC	1500
Qy	1522	AGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGAAATATAAGAGATTTATGAC	1581
Db	1501	AGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGAAATATAAGAGATTTATGAC	1560
Qy	1582	CTTTCAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTTGGAGAAAGGCATC	1641
Db	1561	CTTTCAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTTGGAGAAAGGCATC	1620
Qy	1642	CTTCACAAAGGAAAGCGGAGCCATCAAGCGCATTTATAGCAGCTGTAATAATGGCAA	1701
Db	1621	CTTCACAAAGGAAAGCGGAGCCATCAAGCGCATTTATAGCAGCTGTAATAATGGCAA	1680
Qy	1702	AAGATCCAGGAGTCTTTCACTGTTTTCAGAAAAACATAATATAGCTTAAACACATCTTAAT	1761
Db	1681	AAGATCCAGGAGTCTTTCACTGTTTTCAGAAAAACATAATATAGCTTAAACACATCTTAAT	1740
Qy	1762	TCTGTGATTAATAATTTTGTGACCCCAAGGTTTATTAGAAAGTGCTGAATTTACAGTAGTTA	1821
Db	1741	TCTGTGATTAATAATTTTGTGACCCCAAGGTTTATTAGAAAGTGCTGAATTTACAGTAGTTA	1800
Qy	1822	ACCTTTTACAGTGGTTTAAACATAGCTTTCTCCCGTAAACATATCTGAAAGTAAAGT	1881
Db	1801	ACCTTTTACAGTGGTTTAAACATAGCTTTCTCCCGTAAACATATCTGAAAGTAAAGT	1860
Qy	1882	TGATGTAAAGCTGAGA	1897
Db	1861	TGATGTAAAGCTGAAA	1876

RESULT 14  
 US-10-141-702-89  
 ; Sequence 89, Application US/10141702

Publication No. US20030134358A1  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Beresini, Maureen  
 APPLICANT: DeForge, Laura  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K  
 APPLICANT: Wood, William  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 FILE OF INVENTION: ACIDS ENCODING THE SAME  
 FILE REFERENCE: P3330R1C208  
 CURRENT APPLICATION NUMBER: US/10/141,702  
 CURRENT FILING DATE: 2002-05-08  
 Prior Application removed - See Palm or File Wrapper  
 NUMBER OF SEQ ID NOS: 550  
 SEQ ID NO 89  
 LENGTH: 1893  
 TYPE: DNA  
 ORGANISM: Homo Sapien  
 US-10-141-702-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	22	GTCTCCGCGTCACAGGAATTCAGACCCACAGGGGGGACAGGCTCCCTCTACCTGGA	81
DB	1	GTCTCCGCGTCACAGGAATTCAGACCCACAGGGGGGACAGGCTCCCTCTACCTGGA	60
QY	82	GACTTGACTCCCGCGCGCCCAACCTGCTTTATCCCTTGACGCTCGAGTGTGAGATCC	141
DB	61	GACTTGACTCCCGCGCGCCCAACCTGCTTTATCCCTTGACGCTCGAGTGTGAGATCC	120
QY	142	TGCAGCGCGCGAGTCCCGCGCGCTCTCCCGCCCAACCTGCTTCTGCTCTCTCTGT	201
DB	121	TGCAGCGCGCGAGTCCCGCGCGCTCTCCCGCCCAACCTGCTTCTGCTCTCTCTGT	180
QY	202	TTTTACTCTCTCTTTTCATTCATTAACAAGCTACAGCTCCAGGAGCCCGCGGGGT	261
DB	181	TTTTACTCTCTCTTTTCATTCATTAACAAGCTACAGCTCCAGGAGCCCGCGGGGT	240
QY	262	GTGACCCAAAGCGAGCGTGAAGAATGGGGTTCCTCGGACCGGCACCTTGGATTCTGGTG	321
DB	241	GTGACCCAAAGCGAGCGTGAAGAATGGGGTTCCTCGGACCGGCACCTTGGATTCTGGTG	300
QY	322	TTAGTGCTCCCGATTCAAGCTTTCCCAACCTGAGGAGCCCAAGACAAATCTCTACAT	381
DB	301	TTAGTGCTCCCGATTCAAGCTTTCCCAACCTGAGGAGCCCAAGACAAATCTCTACAT	360
QY	382	AATAGAGATTAAAGTGCAGAAAGCTTTGAATGAACAGTGTGCTGAAGCAGAAAGAC	441
DB	361	AATAGAGATTAAAGTGCAGAAAGCTTTGAATGAACAGTGTGCTGAAGCAGAAAGAC	420
QY	442	AAGATTAATAAACATATCTCCAGAAACAGCGGTCAGAGCAACTATTTCTTTGTT	501
DB	421	AAGATTAATAAACATATCTCCAGAAACAGCGGTCAGAGCAACTATTTCTTTGTT	480
QY	502	GATACTTGAACCTCTTGGGCAATACAGAAAGGAAAAAATTTGAGAAAGACAA	561
DB	481	GATACTTGAACCTCTTAAAGGCAATACAGAAAGGAAAAAATTTGAGAAAGACAA	540
QY	562	TCATATAAGAGCTCCCACTTGATTAATAGTGAATGGAAGTGTGATTCACCAAG	621

Db	541	TCTATAGAAGCTCCCACTTGATTAAGTGAATGGAAGATGTTGATTCACCAAG	600
QY	622	AATCGAAAACCTGATCGATGATTTACTCTACTAAGAGTGGATGATCAATAATTTCAA	681
Db	601	AATCGAAAACCTGATCGATGATTTACTCTACTAAGAGTGGATGATCAATAATTTCAA	660
QY	682	GATGATCCAGATGCTTCACTCACTAGAGGGGACCTTTAAACCCTGAAGCATTTGTC	741
Db	661	GATGATCCAGATGCTTCACTCACTAGAGGGGACCTTTAAACCCTGAAGCATTTGTC	720
QY	742	CATAAAATCGCTCCAGGATTTATGAAGAAATACAGAGCCGCTGTTGACAAGATTTGT	801
Db	721	CATAAAATCGCTCCAGGATTTATGAAGAAATACAGAGCCGCTGTTGACAAGATTTGT	780
QY	802	TCTAAACTACTTAATCTCGGCTTATCACAAGAACCAACACATACACTGGAAGATGAA	861
Db	781	TCTAAACTACTTAATCTCGGCTTATCACAAGAACCAACACATACACTGGAAGATGAA	840
QY	862	GTAGCAGAGGTTTACAAAAATTAATCTCAAGGAAGCCCAACATTTATGAGGAGATCCC	921
Db	841	GTAGCAGAGGTTTACAAAAATTAATCTCAAGGAAGCCCAACATTTATGAGGAGATCCC	900
QY	922	AATAAGCCCAAGCTGGACTGAGAAATCAGGCTGGAAGAAATACAGAGAAAGTGAATCCA	981
Db	901	AATAAGCCCAAGCTGGACTGAGAAATCAGGCTGGAAGAAATACAGAGAAAGTGAATCCA	960
QY	982	ATGGCAGCAATTCAGATGCTTGTCTAAGGGAGAAACAGATGATTAACACACA	1041
Db	961	ATGGCAGCAATTCAGATGCTTGTCTAAGGGAGAAACAGATGATTAACACACA	1020
QY	1042	TTAAACCTTGACAAATGGCTTGAAGGAGAACTTAAACCTTACAGTGAAGACAACTTTAGG	1101
Db	1021	TTAAACCTTGACAAATGGCTTGAAGGAGAACTTAAACCTTACAGTGAAGACAACTTTAGG	1080
QY	1102	GACTTCCAATATTTCCCAATTTCTATGCGCTACTGAAAGATTTGATTGAGAAAGAA	1161
Db	1081	GAACTCCAATATTTCCCAATTTCTATGCGCTACTGAAAGATTTGATTGAGAAAGAA	1140
QY	1162	GCAAAAGAGAAAGAACTGATTAATCATATGAAACACTGATTTGAGATG	1221
Db	1141	GCAAAAGAGAAAGAACTGATTAATCATATGAAACACTGATTTGAGATG	1200
QY	1222	ATGGTGAATATGGAACAAATATCTCAGAAAGAGTGTTCCTTCTTCTTCTTCTTCTTCT	1281
Db	1201	ATGGTGAATATGGAACAAATATCTCAGAAAGAGTGTTCCTTCTTCTTCTTCTTCTTCT	1260
QY	1282	GAAATGATTTGCTTCTCAGACCAAAACAGCTAGAAAAATTTGCTTACTGACAAATATAAGC	1341
Db	1261	GAAATGATTTGCTTCTCAGACCAAAACAGCTAGAAAAATTTGCTTACTGACAAATATAAGC	1320
QY	1342	AAGCTTTTCCCAAGCACTCAGAGAAAGTGTATGAAAGCTTTGAAAGATTTCCACAAAAAGAT	1401
Db	1321	AAGCTTTTCCCAAGCACTCAGAGAAAGTGTATGAAAGCTTTGAAAGATTTCCACAAAAAGAT	1380
QY	1402	GCAGCTAAGATGGAAGAAAGATATGAAAGCTTTGAAAGATTTCCACAAAAAGATATAACCTCC	1461
Db	1381	GCAGCTAAGATGGAAGAAAGATATGAAAGCTTTGAAAGATTTCCACAAAAAGATATAACCTCC	1440
QY	1462	AACCCAGAGGAAAGACAGATGAACCCAAAGAAACAGAGCCCTATTGGAAGCCATC	1521
Db	1441	AACCCAGAGGAAAGACAGATGAACCCAAAGAAACAGAGCCCTATTGGAAGCCATC	1500
QY	1522	AGAAAAATATTTGAATGTTTGAAGAAACATGACAAAAAGGAAATTAAGAGATTTATGAC	1581
Db	1501	AGAAAAATATTTGAATGTTTGAAGAAACATGACAAAAAGGAAATTAAGAGATTTATGAC	1560
QY	1582	CTTTCAAGATGAGAGACTTCAATAAACAAGCTGATGCTTATGTTGAGAAAGGCAATC	1641
Db	1561	CTTTCAAGATGAGAGACTTCAATAAACAAGCTGATGCTTATGTTGAGAAAGGCAATC	1620
QY	1642	CTTGACAGGAGAGGAGCGGCGCATTAAGCGCATTTATAGCAGCTGCTTAAATATGGCAA	1701

Db 1621 CTTGACAGGAAGAGCCGAGGCCATCAAGCCATTTATAGAGCCTGTAAAAAGGCAA 1680  
QY 1702 AAGATCCAGAGTCTTTCAACTGTTTCAGAAAAAATAATATAGCTTAAAAACACTTCTAAT 1761  
Db 1681 AAGATCCAGAGTCTTTCAACTGTTTCAGAAAAAATAATATAGCTTAAAAACACTTCTAAT 1740  
QY 1762 TCTGTGATTAATAATTTTGTGACCCCAAGGGTTATTAGAAAGTCTCTGAATTTACAGTAGTTA 1821  
Db 1741 TCTGTGATTAATAATTTTGTGACCCCAAGGGTTATTAGAAAGTCTCTGAATTTACAGTAGTTA 1800  
QY 1822 ACCTTTTACAAGTGTAAAAACATAGCTTTCTCCCGTAAAAACATCTCTGAAGTAAAGT 1881  
Db 1801 ACCTTTTACAAGTGTAAAAACATAGCTTTCTCCCGTAAAAACATCTCTGAAGTAAAGT 1860  
QY 1882 TGTATGTAAGCTGAGA 1897  
Db 1861 TGTATGTAAGCTGAAA 1876

RESULT 15  
US-10-141-704-89  
; Sequence 89, Application US/10141704  
; Publication No. US20030134359A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C209  
; CURRENT FILING DATE: 2002-05-08  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 89  
; LENGTH: 1893  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-141-704-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 GTCTCGGCTACAGAACTTCAGCACCCACAGGGGGACAGCGTCCCTCTACCTGGA 81  
Db 1 GTCTCGGCTACAGAACTTCAGCACCCACAGGGGGACAGCGTCCCTCTACCTGGA 60  
QY 82 GACTTGTACTCCCGCGCCCAACCTGCTTATCCCTTGACCGTCGAGTGTCTGAGATCC 141  
Db 61 GACTTGTACTCCCGCGCCCAACCTGCTTATCCCTTGACCGTCGAGTGTCTGAGATCC 120  
QY 142 TGCAGCGCCCAAGTCCCGGCCCTCTCCCGCCCAACACCCACCCCTCTGCTTCTCTGT 201  
Db 121 TGCAGCGCCCAAGTCCCGGCCCTCTCCCGCCCAACACCCACCCCTCTGCTTCTCTGT 180  
QY 202 TTTTACTGCTCTCTTTTCAATATACAAAAGTCTACAGTCCAGAGAGCCAGCGCGGCT 261  
Db 181 TTTTACTGCTCTCTTTTCAATATACAAAAGTCTACAGTCCAGAGAGCCAGCGCGGCT 240

QY 262 GTGACCCCAAGCCGAGCGTGGAAAGATGGGGTTCTCGGACCGGCACCTTGGATTCTGTGG 321  
Db 241 GTGACCCCAAGCCGAGCGTGGAAAGATGGGGTTCTCGGACCGGCACCTTGGATTCTGTGG 300  
QY 322 TTATGTCTCCCGATTCAGCTTTCCCAAAACCTCGAGGAAGCAAGACAAATCTCTACAT 381  
Db 301 TTATGTCTCCCGATTCAGCTTTCCCAAAACCTCGAGGAAGCAAGACAAATCTCTACAT 360  
QY 382 AATAGAGATTAAGTGCAGAAAGACCTTTGAATGAACAGATTCCTGAAGCAGAAAGAAC 441  
Db 361 AATAGAGATTAAGTGCAGAAAGACCTTTGAATGAACAGATTCCTGAAGCAGAAAGAAC 420  
QY 442 AAGATTAAAAAACATATCTCTCCAGAAAAACAGCCAGGTCAGAGCAACTATTTCTTTGTT 501  
Db 421 AAGATTAAAAAACATATCTCTCCAGAAAAACAGCCAGGTCAGAGCAACTATTTCTTTGTT 480  
QY 502 GATACTTTGAACCTGCTAAGGCCAATACAGAAAAAGGAAAAAATTTGAGAAAGAACACAA 561  
Db 481 GATACTTTGAACCTGCTAAGGCCAATACAGAAAAAGGAAAAAATTTGAGAAAGAACACAA 540  
QY 562 TCTATAAGNAGCTCCCCACTTGTATATAAGTTGAATGTGGAAGATGTTGATTTCAACCAAG 621  
Db 541 TCTATAAGNAGCTCCCCACTTGTATATAAGTTGAATGTGGAAGATGTTGATTTCAACCAAG 600  
QY 622 AATCGAAAACTGATCGATGATTGATCTACTTAAGTGGATTTGGATCATAAATTTCAA 681  
Db 601 AATCGAAAACTGATCGATGATTGATCTACTTAAGTGGATTTGGATCATAAATTTCAA 660  
QY 682 GATGATCCAGATGGTCTTCACTAGACGGGACTCTTTAACCGCTGAAGACATGTC 741  
Db 661 GATGATCCAGATGGTCTTCACTAGACGGGACTCTTTAACCGCTGAAGACATGTC 720  
QY 742 CATAAATCGCTGCCAGGATTTATGAAGAAATATGACAGAGCGCTGTTTACAGAGATGTT 801  
Db 721 CATAAATCGCTGCCAGGATTTATGAAGAAATATGACAGAGCGCTGTTTACAGAGATGTT 780  
QY 802 TCTAAACTACTTTAATCTCGGCTTATACAGAAAGCCAAAGCACATACACTGGAAGATGAA 861  
Db 781 TCTAAACTACTTTAATCTCGGCTTATACAGAAAGCCAAAGCACATACACTGGAAGATGAA 840  
QY 862 GTAGCAGAGGTTTACAAAAATTAATCTCAAAGGAAGCCAAATATATAGAGGATGCC 921  
Db 841 GTAGCAGAGGTTTACAAAAATTAATCTCAAAGGAAGCCAAATATATAGAGGATGCC 900  
QY 922 AATAAGCCACAAAGCTGGACTGAGATCAGCTGGAAGAAATACAGAGAAAGTGACTCCA 981  
Db 901 AATAAGCCACAAAGCTGGACTGAGATCAGCTGGAAGAAATACAGAGAAAGTGACTCCA 960  
QY 982 ATGGCAGCAATTTCAAGATGGTCTTGTAAAGGAGAAACGATGAACACAGTATCTAACACA 1041  
Db 961 ATGGCAGCAATTTCAAGATGGTCTTGTAAAGGAGAAACGATGAACACAGTATCTAACACA 1020  
QY 1042 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTTAAACCTACAGTGAAGACAACTTTAGG 1101  
Db 1021 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTTAAACCTACAGTGAAGACAACTTTAGG 1080  
QY 1102 GACTTCCATATTTTCCCAATTTCTATGCGCTACTGAAAGATTTGATTTCAGAAAGAA 1161  
Db 1081 GACTTCCATATTTTCCCAATTTCTATGCGCTACTGAAAGATTTGATTTCAGAAAGAA 1140  
QY 1162 GCAAAGAGAGAAAGAACTGATTTACTATCATGAAACACTGATTGACTTTGTGAAGATG 1221  
Db 1141 GCAAAGAGAGAAAGAACTGATTTACTATCATGAAACACTGATTGACTTTGTGAAGATG 1200  
QY 1222 ATGGTGAATATGGAACAAATATCTCCAGAAAGAGTGTTCCTACCTTGAACAACTTTGGAT 1281  
Db 1201 ATGGTGAATATGGAACAAATATCTCCAGAAAGAGTGTTCCTACCTTGAACAACTTTGGAT 1260  
QY 1282 GAAATGATTCCTTCAGACCAAAACAGCTAGAAAAAATGCTACTGACAAATATAGC 1341  
Db 1261 GAAATGATTCCTTCAGACCAAAACAGCTAGAAAAAATGCTACTGACAAATATAGC 1320

Search completed: August 28, 2003, 10:19:44  
Job time : 531 secs







QY 1140 AAGTATGATTCAGAAAAAGCAAAAGAGAAACCTGATTACTATCATATAAAC 1199  
 DB 1154 AAGTATGATTCAGAAAAAGCAAAAGAGAAACCTGATTACTATCATATAAAC 1213  
 QY 1200 ACTGATGACCTTGTGAAGATGATGCTGAATATGCAACATATCTCCAGAAAGAGTGT 1259  
 DB 1214 ACTGATGACCTTGTGAAGATGATGCTGAATATGCAACATATCTCCAGAAAGAGTGT 1273  
 QY 1260 TTCCTACCTGAAAACTTGATGAATGATGCTCTTTCAGACCAAAAAACGCTTGAAAA 1319  
 DB 1274 TTCCTACCTGAAAACTTGATGAATGATGCTCTTTCAGACCAAAAAACGCTTGAAAA 1333  
 QY 1330 AATGCTACTGACATATATAGCAAGCTTTTCCACACACATCAGAGAGAGCATGAGAA 1379  
 DB 1334 AATGCTACTGACATATATAGCAAGCTTTTCCACACACATCAGAGAGAGCATGAGAA 1393  
 QY 1380 AACAGACAGTACCAAGAAAGAGAGCTAGATGAGAAAGAAATATGAGACCTTGAAAGA 1439  
 DB 1394 AACAGACAGTACCAAGAAAGAGAGCTAGATGAGAAAGAAATATGAGACCTTGAAAGA 1453  
 QY 1440 TTCACAAAGATGATTAAGTACCAACCCAGAGAGAAAGACATGACCAAGAGAAAAAC 1499  
 DB 1454 TTCACAAAGATGATTAAGTACCAACCCAGAGAGAAAGACATGACCAAGAGAAAAAC 1513  
 QY 1500 AGAAGCCTATTTGGAGCCATCAGAAAAAATATGAAATGTTGAAGAAACATGACAAAA 1559  
 DB 1514 AGAAGCCTATTTGGAGCCATCAGAAAAAATATGAAATGTTGAAGAAACATGACAAAA 1573  
 QY 1560 GGGAAATTAAGAAAGATTAATGACCTTTCAGAGATGAGAGACTTTCATATAAACAAGCTGA 1619  
 DB 1574 GGGAAATTAAGAAAGATTAATGACCTTTCAGAGATGAGAGACTTTCATATAAACAAGCTGA 1633  
 QY 1620 TGCCTATGTGAGAAAGGATCCTTGACAAAGAAAGCGAGGCCATCAAGCCCATTTA 1679  
 DB 1634 TGCCTATGTGAGAAAGGATCCTTGACAAAGAAAGCGAGGCCATCAAGCCCATTTA 1693  
 QY 1680 TAGCAGCCTGTAATAATGGCAAAAGATCCAGAGACTTTCAGAGCTTTCAGAAAAACATAA 1739  
 DB 1694 TAGCAGCCTGTAATAATGGCAAAAGATCCAGAGACTTTCAGAGCTTTCAGAAAAACATAA 1753  
 QY 1740 TATAGCTTAAACACCTCTAATTTGTGATTAATAATTTTTCAGCCAGGCTTATTAGAA 1799  
 DB 1754 TATAGCTTAAACACCTCTAATTTGTGATTAATAATTTTTCAGCCAGGCTTATTAGAA 1813  
 QY 1800 AGTGTGAAATTCAGAGATTAACCTTTTACAGAGTGTGTAACATAGCTTCTCCCGT 1859  
 DB 1814 AGTGTGAAATTCAGAGATTAACCTTTTACAGAGTGTGTAACATAGCTTCTCCCGT 1873  
 QY 1860 AAAAATATCTGAAAGTAAAGTTGATGATGAGATTTTGTATACAGAAATCTTAT 1919  
 DB 1874 AAAAATATCTGAAAGTAAAGTTGATGATGAGATTTTGTATACAGAAATCTTAT 1932  
 QY 1920 TTCCTACCTGAAAACTTGATGAATGATGCTCTTTCAGACCAAAAAACGCTTGAAAA 1979  
 DB 1933 TTCCTACCTGAAAACTTGATGAATGATGCTCTTTCAGACCAAAAAACGCTTGAAAA 1988  
 QY 1980 TGGGCTGACCCNTAAACATCAATCCNTCTCCACTGTC 2017  
 DB 1989 TGGGCTGACCCNTAAACATCAATCCNTCTCCACTGTC 2024  
 RESULT 3  
 ID AAA96353 standard: cdna; 1893 BP.  
 AC AAA96353;  
 XX 08-FEB-2001 (first entry)  
 DE cdna encoding a novel polypeptide designated PRO5990.  
 XX Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;

KW PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;  
 KW PRO4352; PRO4380; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;  
 KW INSULINEMIA; PRO4422; PRO4430; PRO4499; tumor; obesity; diabetes;  
 KW Insulinemia; kidney disorder; Bergers disease; nephropathy;  
 KW Schonlein-Henoch purpura; celliac disease; dermatitis herpeticiformis;  
 OS Crohns disease; ss.  
 XX Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 265..1671  
 FT FT /\*tag= a  
 XX MO200056889-A2.  
 PD 28-SEP-2000.  
 PF 01-MAR-2000; 2000WO-US05601.  
 PR 23-MAR-1999; 99US-0125774.  
 PR 23-MAR-1999; 99US-0125778.  
 PR 24-MAR-1999; 99US-0125826.  
 PR 31-MAR-1999; 99US-0127035.  
 PR 05-APR-1999; 99US-0127706.  
 PR 21-APR-1999; 99US-0130359.  
 PR 27-APR-1999; 99US-0131270.  
 PR 27-APR-1999; 99US-0131272.  
 PR 27-APR-1999; 99US-0131291.  
 PR 04-MAY-1999; 99US-0132371.  
 PR 04-MAY-1999; 99US-0132379.  
 PR 04-MAY-1999; 99US-0132383.  
 PR 25-MAY-1999; 99US-0135750.  
 PR 08-JUN-1999; 99US-0138166.  
 PR 20-JUL-1999; 99US-0144791.  
 PR 03-AUG-1999; 99US-0146970.  
 PR 09-DEC-1999; 99US-0170262.  
 XX (GENTH ) GENENTECH INC.  
 PA Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;  
 PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI; 2000-628263/60.  
 DR P-SDB; AAB18926.  
 PT Novel secreted and transmembrane polypeptides useful for diagnosing  
 PT tumour in a mammal, for identifying agonists and antagonists of the  
 PT polypeptide and for therapeutic use  
 PS Claim 2; Fig 35; 222pp; English.  
 XX The present sequence encodes a secreted or transmembrane polypeptide.  
 CC The specification describes polypeptides designated PRO1484, PRO4334,  
 CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,  
 CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO4425, PRO5990,  
 CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is  
 CC useful for diagnosing tumour in a mammal. The polypeptides, their  
 CC agonists and antagonists are useful treating a condition associated with  
 CC expression or activity of the polypeptide. Conditions treated include  
 CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are  
 CC capable of inducing proliferation of mammalian kidney mesangial cells  
 CC and are therefore useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Bergers disease or other  
 CC nephropathies associated with Schonlein-Henoch purpura, celliac disease,  
 CC dermatitis herpeticiformis or Crohns disease. The nucleic acids may be used  
 CC to generate transgenic animals for use in development and screening of  
 CC therapeutically useful reagents and also for chromosome identification  
 CC and tissue typing.  
 XX Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other;  
 SO Query Match 92.5%; Score 1866.4; DB 21; Length 1893;  
 Best Local Similarity 99.7%; Pred. NO. 0;



Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	22	GTCTCCGGCTACAGAAACTTCAACACCAAGGGGAGACAGCGTCCCTCTACCTGGA	81
Db	1	GTCTCCGGCTACAGAACTTCAACACCAAGGGGAGACAGCGTCCCTCTACCTGGA	60
QY	82	GACTTGACTCCCGGGGCCCCCAACCCCTGCTTATCCCTTGACCGTGCAGTGCAGATTC	141
Db	61	GACTTGACTCCCGGGGCCCCCAACCCCTGCTTATCCCTTGACCGTGCAGTGCAGATTC	120
QY	142	TGCAAGCCGCCAGTCCCGGGCCCTCTCCGGCCCAACCACTCCTGGCTCTTCTGT	201
Db	121	TGCAAGCCGCCAGTCCCGGGCCCTCTCCGGCCCAACCACTCCTGGCTCTTCTGT	180
QY	202	TTTTTACTCTCTTTTTCATTCATTAACAAAGCTCTACACTCAGAGAGCCCAAGCCGGAGCT	261
Db	181	TTTTTACTCTCTTTTTCATTCATTAACAAAGCTCTACACTCAGAGAGCCCAAGCCGGAGCT	240
QY	262	GTGACCCAGCCGAGCGCTGGAAGATGGGGTTCCTGGGACCGGCACTTGGATCTGTGTG	321
Db	241	GTGACCCAGCCGAGCGCTGGAAGATGGGGTTCCTGGGACCGGCACTTGGATCTGTGTG	300
QY	322	TTTGTGTCTCCGATTCGAAGCTTTTCCCAACCTGGAAGAGCCCAAGCAATCTCTCAT	381
Db	301	TTTGTGTCTCCGATTCGAAGCTTTTCCCAACCTGGAAGAGCCCAAGCAATCTCTCAT	360
QY	382	AATAGAGATTTAAGTGCAGAAAGACCTTTGATGCATACAGATTGCTGGAAGCAAGAGAC	441
Db	361	AATAGAGATTTAAGTGCAGAAAGACCTTTGATGCATACAGATTGCTGGAAGCAAGAGAC	420
QY	442	AAAGTTAAAAAACATATCTCTCCAGAAAACAGCCAGCTCAGAGCACTATCTTTGTT	501
Db	421	AAAGTTAAAAAACATATCTCTCCAGAAAACAGCCAGCTCAGAGCACTATCTTTGTT	480
QY	502	GATTAAGTGAACCGCTAAGGGCAATTAACAGAAAGAGAAAAAATTGAGAAAGAACAA	561
Db	481	GATTAAGTGAACCGCTAAGGGCAATTAACAGAAAGAGAAAAAATTGAGAAAGAACAA	540
QY	562	TCTATAAGAAAGCTCCCACTTGATTAATTAAGTTGATGTGAGATGTTGATTCACCAAG	621
Db	541	TCTATAAGAAAGCTCCCACTTGATTAATTAAGTTGATGTGAGATGTTGATTCACCAAG	600
QY	622	AATGAAAGACTGATGCATGATGATTAAGCTCTACTAAGAGTGGAATGGATCATTAATTCCA	681
Db	601	AATGAAAGACTGATGCATGATGATTAAGCTCTACTAAGAGTGGAATGGATCATTAATTCCA	660
QY	682	GATGATCCAGATGGCTTTCATCAACTAGACGGGAGCTCCTTAAACCGCTGAAGACATTGTC	741
Db	661	GATGATCCAGATGGCTTTCATCAACTAGACGGGAGCTCCTTAAACCGCTGAAGACATTGTC	720
QY	742	CATTAAGTCCGCTGCGCAGGATTTATGAAGAAAAATACAGAGCCGCTTTGACACATTTGT	801
Db	721	CATTAAGTCCGCTGCGCAGGATTTATGAAGAAAAATACAGAGCCGCTTTGACACATTTGT	780
QY	802	TCTAAACTACTTAATCTCGGCTTATATACAGAAAGCCAAAGCACTATACCTGGAAGTGA	861
Db	781	TCTAAACTACTTAATCTCGGCTTATATACAGAAAGCCAAAGCACTATACCTGGAAGTGA	840
QY	862	GTAGCAGAGGTTTACAAAAATTATCTCAAGGAAGCCCAACTTATAGAGAGATGCC	921
Db	841	GTAGCAGAGGTTTACAAAAATTATCTCAAGGAAGCCCAACTTATAGAGAGATGCC	900
QY	922	AATTAAGCCCAACACTGGACTGAAATACAGAGCTGGAAAAATACAGAGAAAGTGAATCCA	981
Db	901	AATTAAGCCCAACACTGGACTGAAATACAGAGCTGGAAAAATACAGAGAAAGTGAATCCA	960
QY	982	ATGGCAGCAATTCAAGATGCTCTTGCTAAGGGAGAAAAAGATGGAAGATGTTCTAACACA	1041
Db	961	ATGGCAGCAATTCAAGATGCTCTTGCTAAGGGAGAAAAAGATGGAAGATGTTCTAACACA	1020
QY	1042	TTTAACCTTGACAAATGGCTTGGAAGAGAACTTAAACCTTACAGTGAAGACACTTTAGG	1101
Db	1021	TTTAACCTTGACAAATGGCTTGGAAGAGAACTTAAACCTTACAGTGAAGACACTTTAGG	1080

QY	1102	GAC TTC CCA AT AT TT TCC CAA AT TT TCT AT GCG C TACT GAA A A C AT TT AT G AT TC G A A A A A A A A A	1161
Db	1081	GAAC TCC AAT AT TT TCC CAA AAT TT TCT AT GCG C TACT GAA A A C AT TT AT G AT TC G A A A A A A A A A	1140
QY	1162	GCA A A A G A G A A A A A A C A C T G A T T A C T A T C A T G A A A A C A C T G A T T G A A G A T G	1221
Db	1141	GCA A A A G A G A A A A A A C A C T G A T T A C T A T C A T G A A A A C A C T G A T T G A A G A T G	1200
QY	1222	AT G T G A A A T A T A T G A A C A A T A T C T C A G A A G A G T G T T T C T A C T T G A A A C T T G G A T	1281
Db	1201	AT G T G A A A T A T A T G A A C A A T A T C T C A G A A A G A G T G T T T C T A C T T G A A A C T T G G A T	1260
QY	1282	G A A T T G A T T G C T C T T C A G A C C A A A A A C A G A G T A G A A A A A A A A T T G T A C T A G A A A T A T A G C	1341
Db	1261	G A A T T G A T T G C T C T T C A G A C C A A A A A C A G A G T A G A A A A A A A A T T G T A C T A G A A A T A T A G C	1320
QY	1342	A A G C T T T T C C C A G A C A C A T C A G A A G A G T A T G A A A A C A G A C A G A T T A C C A A G A A G A A	1401
Db	1321	A A G C T T T T C C C A G A C A C A T C A G A A G A G T A T G A A A A C A G A C A G A T T A C C A A G A A G A A	1380
QY	1402	G C A G C T A A G A T G A A A A G A A T A T G A A G C T T T G A A G A T T C C A C A A A A G A T A T A C T C	1461
Db	1381	G C A G C T A A G A T G A A A A G A A T A T G A A G C T T T G A A G A T T C C A C A A A A G A T A T A C T C	1440
QY	1482	A A C C C A G A G A A A A C A G A T A G A A C C C A A A G A A A A A C A G A A G C T A T T T G A A G C C A T C	1521
Db	1441	A A C C C A G A G A A A A C A G A T A G A A C C C A A A G A A A A A C A G A A G C T A T T T G A A G C C A T C	1500
QY	1522	A G A A A A A A T A T T G A T G G T T G A G A A A C A T G A C A A A A A G G A A A T A A A G A A T T A T G A C	1581
Db	1501	A G A A A A A A T A T T G A T G G T T G A G A A A C A T G A C A A A A A G G A A A T A A A G A A T T A T G A C	1560
QY	1582	C T T T C A A A G A T A G A G A C T T C A T C A A T A A C A A G C T G A T G C T T A T G T G A A A A G C A T C	1641
Db	1561	C T T T C A A A G A T A G A G A C T T C A T C A A T A A C A A G C T G A T G C T T A T G T G A A A A G C A T C	1620
QY	1642	C T T G C A A G A A A A G C C G A G C C A T C A A G C C A T T T T A C A G C C T G A A A A A T G C C A	1701
Db	1621	C T T G C A A G A A A A G C C G A G C C A T C A A G C C A T T T T A C A G C C T G A A A A A T G C C A	1680
QY	1702	A A G A T C A G A G A C T C T T T C A C T G T T T C A G A A A A C A A T A A T A G C T T A A A C A C T T T A T	1761
Db	1681	A A G A T C A G A G A C T C T T T C A C T G T T T C A G A A A A C A A T A A T A G C T T A A A C A C T T T A T	1740
QY	1762	T C T G T G A T T A A A T T T T T T G A C C C A A G C G T A T T A G A A A G C G A A T T T A C A G A G T T A	1821
Db	1741	T C T G T G A T T A A A T T T T T T T G A C C C A A G C G T A T T A G A A A G C G A A T T T A C A G A G T T A	1800
QY	1822	A C C T T T T C A A G T G T T A A A C A T A G C T T T T C C C G T A A A A A C T A T C T G A A A G T A A G T	1881
Db	1801	A C C T T T T C A A G T G T T A A A C A T A G C T T T T C C C G T A A A A A C T A T C T G A A A G T A A G T	1860
QY	1882	T G T A T G T A A G C T G A A	1897
Db	1861	T G T A T G T A A G C T G A A	1876
RESULT 4			
AAS21288			
ID	AAS21288 standard; cDNA; 1893 BP.		
XX	AAS21288;		
XX	24-OCT-2001 (first entry)		
DE	Human cDNA sequence encoding for PRO5990 polypeptide.		
KW	Human secretory and transmembrane; PRO; mammalian; cancer; lung;		
KW	breast; prostate; cervical; tumor necrosis factor-alpha; TNF-alpha;		
KW	catalyze; eat; proliferation; glucose; free fatty acid; skeletal muscle;		
KW	adipocyte; A-peptide; factor VIIA; gene therapy; ss.		
XX			

OS Homo sapiens.  
 XX  
 PN WO200140466-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000WO-US32678.  
 XX  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14944.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 10-NOV-2000; 2000WO-US30873.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 F1 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 P1 Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 P1 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 WI: 2001-408281/43.  
 P-PSDB: AMU12216.  
 DR  
 DR Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO-polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical  
 XX  
 PS Claim 3; Fig 89; 813pp; English.  
 XX  
 XX AAS2144-AAS21518 encode for novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, the release of a cytokine from peripheral blood  
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.  
 CC  
 XX

SQ Sequence 1893 BP: 698 A; 389 C; 385 G; 421 T; 0 other:  
 Query Match 92.5%; Score 1866.4; DB 22; Length 1893;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 22 GTCTCCGCGTCACAGAACTTCAAGACCCACAGGCGGAGAGCGCTCCCTTACCTGGA 81  
 DB 1 GTCTCCGCGTCACAGAACTTCAAGACCCACAGGCGGAGAGCGCTCCCTTACCTGGA 60  
 QY 82 GACTTGACTCCCGCGGCGCCCAACCCCTTATCCCTTGACCGCTGCTGAGAGATCC 141  
 DB 61 GACTTGACTCCCGCGGCGCCCAACCCCTTATCCCTTGACCGCTGCTGAGAGATCC 120  
 QY 142 TGCAGCGCGCCAGTCCCGGCGCCCTTCCCGCCACACCCACCTCTGCTCTCTGT 201  
 DB 121 TGCAGCGCGCCAGTCCCGGCGCCCTTCCCGCCACACCCACCTCTGCTCTCTGT 180  
 QY 202 TTTTACTCCCTCTTTCATTCATTAACAAAAGCTACAGCTCCAGAGCCCGCGGCT 261  
 DB 181 TTTTACTCCCTCTTTCATTCATTAACAAAAGCTACAGCTCCAGAGCCCGCGGCT 240  
 QY 262 GTGACCCAGCCGAGCGGTGAAGATGGGGTTCCTCGGACCGGCACTTGATTCTGTG 321  
 DB 241 GTGACCCAGCCGAGCGGTGAAGATGGGGTTCCTCGGACCGGCACTTGATTCTGTG 300  
 QY 322 TTAGTCTCCCGATTTACAGTTTCCCAACCTGAGAGAACCAAGCAATCTTACAT 381  
 DB 301 TTAGTCTCCCGATTTACAGTTTCCCAACCTGAGAGAACCAAGCAATCTTACAT 360  
 QY 382 AATAGAGATTAAAGTCAGAAAGACCTTGAATGAACAGATTCTGAGAGAAAGAAC 441  
 DB 361 AATAGAGATTAAAGTCAGAAAGACCTTGAATGAACAGATTCTGAGAGAAAGAAC 420  
 QY 442 AAGATTAAAAAACAATATCTCCAGAAAAACAACCGAGTCAGAGCAACTATCTTGT 501  
 DB 421 AAGATTAAAAAACAATATCTCCAGAAAAACAACCGAGTCAGAGCAACTATCTTGT 480  
 QY 502 GATTAACCTTAACCTGTAGAGCAATTAACAGAAAGAAAAATTAGAAAGAACAA 561  
 DB 481 GATTAACCTTAACCTGTAGAGCAATTAACAGAAAGAAAAATTAGAAAGAACAA 540  
 QY 562 TCTATAAGAGCTCCCACTGTATATAAGTTGAATGGAAGATTATTCACCAAG 621  
 DB 541 TCTATAAGAGCTCCCACTGTATATAAGTTGAATGGAAGATTATTCACCAAG 600  
 QY 622 AATCGAAAATGATGATATATGACTTACTAGAGTGATGATCAATTAATTCAA 681  
 DB 601 AATCGAAAATGATGATATATGACTTACTAGAGTGATGATCAATTAATTCAA 660  
 QY 682 GATGATCCGATGTCCTTCATCACTAGACGGGAGCTCTTAAACGCGTGAACATTTGC 741  
 DB 661 GATGATCCGATGTCCTTCATCACTAGACGGGAGCTCTTAAACGCGTGAACATTTGC 720  
 QY 742 CATTAATTCGTCGCGAGATTATAGAAAATGACAGAGCCGCTGTTGACAAATTTGT 801  
 DB 721 CATTAATTCGTCGCGAGATTATAGAAAATGACAGAGCCGCTGTTGACAAATTTGT 780  
 QY 802 TCTAAACTACTTAATCTGGCGCTTATCAAGAAAGCAACATACATGGAATGAA 861  
 DB 781 TCTAAACTACTTAATCTGGCGCTTATCAAGAAAGCAACATACATGGAATGAA 840  
 QY 862 GTAGAGAGGTTTTCAAAAATTAATTCAAAGAACCAACATTTATGAGAGATGCC 921  
 DB 841 GTAGAGAGGTTTTCAAAAATTAATTCAAAGAACCAACATTTATGAGAGATGCC 900  
 QY 922 AATAAGCCCAAGCTGAGTGAATGAGATGAGCTGGAATAATTCAGAGAAATGACTCA 981  
 DB 901 AATAAGCCCAAGCTGAGTGAATGAGATGAGCTGGAATAATTCAGAGAAATGACTCA 960  
 QY 982 ATGGAGCAATTCAGATGCTTCTTAAGGAGAAAGATGAACAGATATCTAACACA 1041  
 DB 961 ATGGAGCAATTCAGATGCTTCTTAAGGAGAAAGATGAACAGATATCTAACACA 1020

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OY 1042 TTAACCTTGACAAATGGCTGGAAAGAGAACTAAACCTACAGTGAAGACACTTTAGC 1101
DB 1021 TTAACCTTGACAAATGGCTGGAAAGAGAACTAAACCTACAGTGAAGACACTTTAGC 1080
OY 1102 GACTTCCAAATATTTCCCAATTTCTATGCGCTACTGAAAGATATTGATTCAGAAAGAA 1161
DB 1081 GAATCCCAATATTTCCCAATTTCTATGCGCTACTGAAAGATATTGATTCAGAAAGAA 1140
OY 1162 GCAAAAGAGAAAGAAACACTGATTACTATCATGAACACAGTATTGACTTGTGAAGATG 1221
DB 1141 GCAAAAGAGAAAGAAACACTGATTACTATCATGAACACAGTATTGACTTGTGAAGATG 1200
OY 1222 ATGGGAATATGGAACATATCTCCAGAGAGAGGTGTTCTTACTTGAAGAACTTGAT 1281
DB 1201 ATGGGAATATGGAACATATCTCCAGAGAGAGGTGTTCTTACTTGAAGAACTTGAT 1260
OY 1282 GAAATGATTTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAATGCTACTGACATATTAAGC 1341
DB 1261 GAAATGATTTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAATGCTACTGACATATTAAGC 1320
OY 1342 AAGCTTTTCCAGACCAATCATAGAGAGAGTCAATGAAGAACAGACAGTACCAAGAGAA 1401
DB 1321 AAGCTTTTCCAGACCAATCATAGAGAGAGTCAATGAAGAACAGACAGTACCAAGAGAA 1380
OY 1402 GCAGTAGATGGAAGAAAGAAATATGAGAGCTTGAAGATTCACAAAGATGATTAAGTCC 1461
DB 1381 GCAGTAGATGGAAGAAAGAAATATGAGAGCTTGAAGATTCACAAAGATGATTAAGTCC 1440
OY 1462 AACCCAGAGAGAAAGACAGATGAACCCCAAGAAAGAAAGCTATTTGGAGCCATCC 1521
DB 1441 AACCCAGAGAGAAAGACAGATGAACCCCAAGAAAGAAAGCTATTTGGAGCCATCC 1500
OY 1522 AGAAAAATATTTGAATGTTGAAGAAACATGACAAAAAGGAATTAAGATTATGAC 1581
DB 1501 AGAAAAATATTTGAATGTTGAAGAAACATGACAAAAAGGAATTAAGATTATGAC 1560
OY 1582 CTTTCAAGATGAGAGACTTATCATTAATAACAAGTGTATGTTATGTGAGAAAGCATC 1641
DB 1561 CTTTCAAGATGAGAGACTTATCATTAATAACAAGTGTATGTTATGTGAGAAAGCATC 1620
OY 1642 CTTGCAAGAGAAAGCCGAGCCATCAAGCCATTTATGAGAGCCCTGTAATAATGGCA 1701
DB 1621 CTTGCAAGAGAAAGCCGAGCCATCAAGCCATTTATGAGAGCCCTGTAATAATGGCA 1680
OY 1702 AAGATCCAGAGTCTTCACTGTTTCAGAAAACTAATATAGCTTAATAACACTTCTAAT 1761
DB 1681 AAGATCCAGAGTCTTCACTGTTTCAGAAAACTAATATAGCTTAATAACACTTCTAAT 1740
OY 1762 TCTGTGATTAATAATTTTGAACCCAGAGGTATATGAAGAGTCTAATTTACAGTAGTTA 1821
DB 1741 TCTGTGATTAATAATTTTGAACCCAGAGGTATATGAAGAGTCTAATTTACAGTAGTTA 1800
OY 1822 ACCTTTTCAGAGTGTAAACATPAGCTTTCTCCCGTAATAAACTATCTGAAGTAAGT 1881
DB 1801 ACCTTTTCAGAGTGTAAACATPAGCTTTCTCCCGTAATAAACTATCTGAAGTAAGT 1860
OY 1882 TGTATGTAGCTGAGA 1897
DB 1861 TGTATGTAGCTGAGA 1876

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RESULT 5  
AA92132  
ID AAF92132 standard; cDNA; 1893 BP.

XX AAF92132;  
XX 15-MAY-2001 (first entry)  
XX Human PRO5990 cDNA.  
XX Human; PRO protein; mapping; ss.

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XX OS Homo sapiens.
XX PN WO200116318-A2.
XX PD 08-MAR-2001.
XX PF 24-AUG-2000; 2000MO-US23328.
XX PR 01-SEP-1999; 99MO-US20111.
XX PR 15-SEP-1999; 99MO-US21090.
XX PR 07-DEC-1999; 99US-0169495.
XX PR 09-DEC-1999; 99US-0170262.
XX PR 11-JAN-2000; 2000US-0175481.
XX PR 18-FEB-2000; 2000MO-US04341.
XX PR 18-FEB-2000; 2000MO-US04342.
XX PR 22-FEB-2000; 2000MO-US04414.
XX PR 01-MAR-2000; 2000MO-US05601.
XX PR 03-MAR-2000; 2000MO-US187202.
XX PR 25-APR-2000; 2000US-0199397.
XX PR 22-MAY-2000; 2000MO-US14042.
XX PR 05-JUN-2000; 2000US-0209832.
XX PA (GENETH ) GENENTECH INC.
XX PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX DR WPI; 2001-183260/18.
XX DR P-PSDB; AAB87600.
XX PT Eighty four nucleic acids encoding PRO polypeptides, useful in
XX PT molecular biology, including use as hybridization probes, and in
XX PT chromosome and gene mapping.
XX PS Claim 2; Fig 149; 278bp; English.
XX CC The present sequence is the coding sequence for a human PRO polypeptide
XX CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
XX CC antagonists or anti-PRO antibodies are useful for preparation of a
XX CC medicament useful in the treatment of a condition which is responsive to
XX CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
XX CC protein may also be employed as molecular weight markers for protein
XX CC electrophoresis. The PRO coding sequence has applications in molecular
XX CC biology, including use as hybridisation probes, and in chromosome and
XX CC gene mapping.
XX SO Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other;

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Query Match 92.5%; Score 1866.4; DB 22; Length 1893;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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OY 22 GTCCTCGGTCACAGAACTTCAGACCCACAGGCGGAGACGGCTCCCTTACTCTGA 81
DB 1 GTCTCGGTCACAGAACTTCAGACCCACAGGCGGAGACGGCTCCCTTACTCTGA 60
OY 82 GACTTGACTCCGCGCGGCCCAACCCCTGTTATCCCTTGGACCGTGCAGTGCAGATCC 141
DB 61 GACTTGACTCCGCGCGGCCCAACCCCTGTTATCCCTTGGACCGTGCAGTGCAGATCC 120
OY 142 TGCAGCGCCCAAGTCCGCGGCCCTTCCCGCCCAACCCACCCCTCTGCGCTTCTCTGT 201
DB 121 TGCAGCGCCCAAGTCCGCGGCCCTTCCCGCCCAACCCACCCCTCTGCGCTTCTCTGT 180
OY 202 TTTTATCTCTCTCTTTTCAATATACAAAGTACAGTCCAGAGAGCCAGCGCGGCT 261
DB 181 TTTTATCTCTCTCTTTTCAATATACAAAGTACAGTCCAGAGAGCCAGCGCGGCT 240
OY 262 GTGACCAAGCGGAGCGTGAAGAAATGGGTTCTCGGAGACCGGCACTTGGATTCTGCTG 321
DB 241 GTGACCAAGCGGAGCGTGAAGAAATGGGTTCTCGGAGACCGGCACTTGGATTCTGCTG 300

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Qy	322	TTATGCTCCCGATTTCAAGCTTTTCCCAAACTGGAGAGCCAAAGCAAACTCTACAT	381
Db	301	TTATGCTCCCGATTTCAAGCTTTTCCCAAACTGGAGAGCCAAAGCAAACTCTACAT	360
Qy	382	AATGAGAAATTAAGTCGAGAAAGACCTTTGAATGAACAGATGTGCGAGAGAAAGAAC	441
Db	361	AATGAGAAATTAAGTCGAGAAAGACCTTTGAATGAACAGATGTGCGAGAGAAAGAAC	420
Qy	442	AAGTTAAAAAACATATCTCCAGAAACCAAGCCAGTCAGAGCAATATCTTTGGTT	501
Db	421	AAGTTAAAAAACATATCTCCAGAAACCAAGCCAGTCAGAGCAATATCTTTGGTT	480
Qy	502	GATAACTTGAACCTGCTTAAGGCAATTAACGAAAAGGAAAAAATTGAGAAAGAAACACA	561
Db	481	GATAACTTGAACCTGCTTAAGGCAATTAACGAAAAGGAAAAAATTGAGAAAGAAACACA	540
Qy	562	TCATAAAGAACTCCCACTTGATTAATTAAGTTGAATGTGGAAGATTTGATTCACCAAG	621
Db	541	TCATAAAGAACTCCCACTTGATTAATTAAGTTGAATGTGGAAGATTTGATTCACCAAG	600
Qy	622	AATCGAAAACGTAGATGATTTATGACTCTACTAAGAGTGGATTTGATTCATAATTTCAA	681
Db	601	AATCGAAAACGTAGATGATTTATGACTCTACTAAGAGTGGATTTGATTCATAATTTCAA	660
Qy	682	GATGATCCAGATGGCTTTCATCACTAGACGGGACTCCTTAAACGCTGAAGCAATTTGC	741
Db	661	GATGATCCAGATGGCTTTCATCACTAGACGGGACTCCTTAAACGCTGAAGCAATTTGC	720
Qy	742	CATAAATATGCTGCCGAGATTTATGAAAGAAATGACAGAGCCGTGTTTACAAAGATTTG	801
Db	721	CATAAATATGCTGCCGAGATTTATGAAAGAAATGACAGAGCCGTGTTTACAAAGATTTG	780
Qy	802	TCATAACTATTAATTCGGCCTTATCACAGAAAGCCAAAGCAATACACTGGAAAGTGA	861
Db	781	TCATAACTATTAATTCGGCCTTATCACAGAAAGCCAAAGCAATACACTGGAAAGTGA	840
Qy	862	GTAGCAGAGTTTTCAAAAATTAATTCGCAAGGAAAGCCACAATTTATGAGAGATCCC	921
Db	841	GTAGCAGAGTTTTCAAAAATTAATTCGCAAGGAAAGCCACAATTTATGAGAGATCCC	900
Qy	922	AATTAAGCCCAAGAGCTGAGACTGAGATCAGGCTGGAAAAATACAGAGAAATGACTCCA	981
Db	901	AATTAAGCCCAAGAGCTGAGACTGAGATCAGGCTGGAAAAATACAGAGAAATGACTCCA	960
Qy	982	ATGGGAGCAATTCAGATGTGCTTCTTAAGGAGAAACAGATGAACATATTAACACA	1041
Db	961	ATGGGAGCAATTCAGATGTGCTTCTTAAGGAGAAACAGATGAACATATTAACACA	1020
Qy	1042	TTAACTTGCACAAATGGCTTGGAAAGAGAACTAAACCTACAGTGAAGACAACTTTAG	1101
Db	1021	TTAACTTGCACAAATGGCTTGGAAAGAGAACTAAACCTACAGTGAAGACAACTTTAG	1080
Qy	1102	GACTTCCCAATATTTCCCAATTTCTATGCGCTACTGAAAAGTATTGATTGACGAAAAA	1161
Db	1081	GACTTCCCAATATTTCCCAATTTCTATGCGCTACTGAAAAGTATTGATTGACGAAAAA	1140
Qy	1162	GCAAAAGAGAAAAGAAACACTGTTTCTATCAATGAAAACACGATTTGATTTGTAAGTG	1221
Db	1141	GCAAAAGAGAAAAGAAACACTGTTTCTATCAATGAAAACACGATTTGATTTGTAAGTG	1200
Qy	1222	ATGCTGAATAATGGAACAATATCTCCAGAAAGAGGTGTTTCTACTTTGAAGAACTGGAT	1281
Db	1201	ATGCTGAATAATGGAACAATATCTCCAGAAAGAGGTGTTTCTACTTTGAAGAACTGGAT	1260
Qy	1282	GAAATGATTTGCTCTTCAGACCAAAAACAAAGCTAGAAAAAAATGCTACTGACATATAGC	1341
Db	1261	GAAATGATTTGCTCTTCAGACCAAAAACAAAGCTAGAAAAAAATGCTACTGACATATAGC	1320
Qy	1342	AAGCTTTTCCAGCAGCATCAGAGAAAGTATGAAGAAACAGACAGTACCAGAGAGAA	1401
Db	1321	AAGCTTTTCCAGCAGCATCAGAGAAAGTATGAAGAAACAGACAGTACCAGAGAGAA	1380
Qy	1402	GCACCTAAGATGCAAAAAGAAATATGAAAGCTTGAAGATTCACAAAAAGATGATTAATCC	1461

D	b		 1381 GCAGCTAAGATGTAAGAAGCAATATGGAAAGCTTGAAGGATTCCACAAAAGATGATTAACCTC 1440
Q	y		1462 AACCCGAGGAGGAAGAACACATATAACCCAAAGSAAAAACAAGAGCCATTTTGGAAGCATC 1521
D	b		1441 AACCCTGAGGAGGAAGACAGATTAACCCCAAAGSAAAAACAAGAGCCATTTTGGAAGCATC 1500
Q	y		1522 AGAAAAAATATTGAATGGTTGAAGAACAATGCACAAAAGGGAATATAAGAAAGATTATGAC 1581
D	b		1501 AGAAAAAATATTGAATGGTTGAAGAACAATGCACAAAAGGGAATATAAGAAAGATTATGAC 1560
Q	y		1582 CTTTCAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATC 1641
D	b		1561 CTTTCAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATC 1620
Q	y		1642 CTTGACAAGGAAGAGCGGAGGCCATCAAGGCGATTTATACACGCTGTAAAAATGGCAA 1701
D	b		1621 CTTGACAAGGAAGAGCGGAGGCCATCAAGGCGATTTATACACGCTGTAAAAATGGCAA 1680
Q	y		1702 AAGATCCAGAGCTCTTTCACACTGTTTCGAAAAACATATAATAGTTTAAACACTTCTAAT 1761
D	b		1681 AAGATCCAGAGCTCTTTCACACTGTTTCGAAAAACATATAATAGTTTAAACACTTCTAAT 1740
Q	y		1762 TCTGTGATTAATAATTTTTTGACCCCAAGGCTTATAGAAGTGGAGATTACAGTAGTAA 1821
D	b		1741 TCTGTGATTAATAATTTTTTGACCCCAAGGCTTATAGAAGTGGAGATTACAGTAGTAA 1800
Q	y		1822 ACCCTTTACAGCTGTTTAAACATAGCTTTCTCCGTAAAAACCTATCTGAAGATAAGT 1881
D	b		1801 ACCCTTTACAGCTGTTTAAACATAGCTTTCTCCGTAAAAACCTATCTGAAGATAAGT 1860
Q	y		1882 TGTATGTAAAGCTGAGA 1897 
D	b		1861 TGTATGTAAAGCTGAGA 1876 
			RESULT 6
			ABST74452
ID	ABST74452	standard; cDNA; 1893 BP.	
XX	AC	ABST74452;	
XX	DT	10-DEC-2002 (first entry)	
DE	XX	Human cDNA encoding secreted/transmembrane protein PRO5990.	
XX	XX		
KM	XX	Human; ss; gene; secreted protei; transmembrane protein; antirheumatic;	
KW	XX	antiarthritis; osteopathic; sports-related joint problem;	
XX	XX	articular cartilage defect; osteoarthritis; rheumatoid arthritis.	
OS	XX	Homo sapiens.	
XX	XX		
PX	PN	US2002119130-A1.	
PD	PD	29-AUG-2002.	
PF	XX	06-DEC-2001; 2001US-0006867.	
PR	XX		
PR	XX	29-OCT-1997; 97US-063435P.	
PR	XX	29-OCT-1997; 97US-064215P.	
PR	XX	22-APR-1998; 98US-082797P.	
PR	XX	29-APR-1998; 98US-083495P.	
PR	XX	15-MAY-1998; 98US-085579P.	
PR	XX	10-JUN-1998; 98US-088811P.	
PR	XX	10-JUN-1998; 98US-088824P.	
PR	XX	11-JUN-1998; 98US-088863P.	
PR	XX	12-JUN-1998; 98US-089105P.	
PR	XX	16-JUN-1998; 98US-089514P.	
PR	XX	16-SEP-1998; 98WO-US19330.	
PR	XX	08-MAR-1999; 99WO-US05028.	
PR	XX	14-MAY-1999; 99WO-US10733.	
PR	XX	02-JUN-1999; 99WO-US12252.	

PR 01-SEP-1999: 99MO-US20111.  
 PR 15-SEP-1999: 99MO-US21090.  
 PR 15-SEP-1999: 99MO-US21194.  
 PR 22-DEC-1999: 99MO-US30720.  
 PR 18-FEB-2000: 2000MO-US04341.  
 PR 18-FEB-2000: 2000MO-US04342.  
 PR 30-MAR-2000: 2000MO-US08439.  
 PR 22-MAY-2000: 2000MO-US14042.  
 PR 02-JUN-2000: 2000MO-US15264.  
 PR 23-AUG-2000: 2000MO-US23522.  
 PR 24-AUG-2000: 2000MO-US23328.  
 PR 10-NOV-2000: 2000MO-US30873.  
 PR 01-DEC-2000: 2000MO-US32378.  
 PR 20-DEC-2000: 2000MO-US34956.  
 PR 28-FEB-2001: 2001MO-US06520.  
 PR 20-JUN-2001: 2001MO-US19692.  
 PR 29-JUN-2001: 2001MO-US21066.  
 PR 09-JUL-2001: 2001MO-US21735.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Eston DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 XX  
 DR WPI: 2002-731348/79.  
 DR P-PSDB: ABG95925.  
 PT  
 PT New isolated secreted and transmembrane PRO polypeptide useful for  
 PT modulating biological activity of a cell, or for treating  
 PT sports-related joint problems, osteoarthritis or rheumatoid arthritis  
 XX  
 PS Claim 2; Fig 149; 399pp; English.  
 XX  
 CC The invention relates to an isolated secreted and transmembrane PRO  
 CC polypeptide having 80 % sequence identity to a sequence appearing  
 CC as ABG95851-ABG95934 or their associated signal peptide, or a sequence of  
 CC an extracellular domain of the proteins with their associated signal  
 CC peptide or lacking its associated signal peptide. Also included are  
 CC the nucleic acids encoding the proteins, vectors, host cells,  
 CC fusion proteins and antibodies which specifically bind to the proteins.  
 CC The proteins are useful for detecting a polypeptide designated as A, B, C  
 CC or D in a sample suspected of containing an A, B, C or D polypeptide,  
 CC by contacting the sample with a polypeptide designated as E, F, G, H or  
 CC I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H  
 CC or D/I polypeptide conjugate in the sample, where the formation of the  
 CC conjugate is indicative of the presence of an A, B, C or D polypeptide  
 CC in the sample, where A is a PRO10096 polypeptide, B is a PRO20110  
 CC polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,  
 CC E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040  
 CC polypeptide, H is a PRO20233 polypeptide and I is a PRO1890  
 CC polypeptide. The sample comprises a cell suspected of expressing the A,  
 CC B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with  
 CC a detectable label or is attached to a solid support. The proteins are  
 CC useful for linking a bioactive molecule to a cell expressing a  
 CC polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive  
 CC molecule is a toxin, a radiolabel or an antibody. The bioactive molecule  
 CC causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies  
 CC against them are useful for modulating a biological activity of a cell  
 CC expressing a polypeptide designated as A, B, C or D or E, F, G, H, or  
 CC I. The cell is killed. The proteins are useful for identifying  
 CC agonists or antagonists, for the preparation of a medicament useful in  
 CC the treatment of a condition which is responsive to the proteins, as  
 CC molecular weight markers for protein electrophoresis purposes, and as  
 CC therapeutic agents for treating sports-related joint problems,  
 CC articular cartilage defects, osteoarthritis or rheumatoid arthritis.  
 CC Nucleic acids encoding the proteins are useful as hybridisation probes,  
 CC in chromosome and gene mapping, in the generation of anti-sense RNA and  
 CC DNA, for the preparation of the proteins, to generate transgenic or  
 CC knockout animals which are useful in the development and screening of  
 CC therapeutic useful reagents, for chromosome identification, and in gene  
 CC therapy. The antibody is useful as a therapeutic agent, in a diagnostic  
 CC assay and for affinity purification of the protein from recombinant  
 CC cell culture natural sources. The present sequence encodes a novel

CC secreted or transmembrane protein of the invention.  
 XX  
 SO Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other;  
 Query Match 92.5%; Score 1866.4; DB 24; Length 1893;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 22 GTCGCCGCTCAGACGAACTTACAGACCCACAGGCGGAGACGCCCTCCCTACCTGGA 81  
 DB 1 GTCGCCGCTCAGACGAACTTACAGACCCACAGGCGGAGAGCCCTCCCTACCTGGA 60  
 QY 82 GACTTGACTCCCGGGCGCCCAACCCGCTTATCCCTTGACCCGCTGACAGATGCC 141  
 DB 61 GACTTGACTCCCGGGCGCCCAACCCGCTTATCCCTTGACCCGCTGACAGATGCC 120  
 QY 142 TGCAGCCGCGCAGTCCCGGCCCTCTCCGCCGCCACACCCACCCCTCCCTGCTTCCGT 201  
 DB 121 TGCAGCCGCGCAGTCCCGGCCCTCTCCGCCGCCACACCCACCCCTCCCTGCTTCCGT 180  
 QY 202 TTTTACCTCTCTCTTTCATTAACAAGCTACAGCTCCAGAGCCACGCGCGGCT 261  
 DB 181 TTTTACCTCTCTCTTTCATTAACAAGCTACAGCTCCAGAGCCACGCGCGGCT 240  
 QY 262 GTGACCCCAAGCCGCGGCTGGAAGATGGGCTTCTCCGGAGCCGCGACTTGATTCGTG 321  
 DB 241 GTGACCCCAAGCCGCGGCTGGAAGATGGGCTTCTCCGGAGCCGCGACTTGATTCGTG 300  
 QY 322 TTAGTCTCCGATTCAGGCTTTCCCAACCTGGAGAGCCCAAAATCTCTACAT 381  
 DB 301 TTAGTCTCCGATTCAGGCTTTCCCAACCTGGAGAGCCCAAAATCTCTACAT 360  
 QY 382 AATAGAGAAATTAAGTGAAGAAGACCTTGAATGACAGATTCGTGAAGAGAAAGAC 441  
 DB 361 AATAGAGAAATTAAGTGAAGAAGACCTTGAATGACAGATTCGTGAAGAGAAAGAC 420  
 QY 442 AAGATTAAAAAATATCTCCGAAAGAACAGCAGGAGTCCAGCAACTATCTTTGTT 501  
 DB 421 AAGATTAAAAAATATCTCCGAAAGAACAGCAGGAGTCCAGCAACTATCTTTGTT 480  
 QY 502 GATACCTTGAACCTGCTTAAGGCGCAATTAACAGAAAAAGAAAAATTTGAAAAAGACAA 561  
 DB 481 GATACCTTGAACCTGCTTAAGGCGCAATTAACAGAAAAAGAAAAATTTGAAAAAGACAA 540  
 QY 562 TCTATGAAGAGCTCCCACTTGATTAATGATGATGATGATGATGATGATGATGATGAT 621  
 DB 541 TCTATGAAGAGCTCCCACTTGATTAATGATGATGATGATGATGATGATGATGATGAT 600  
 QY 622 AATGAAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 681  
 DB 601 AATGAAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 QY 682 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 741  
 DB 661 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720  
 QY 742 CATTAATTCGCTGCGAGATTTTGAAGAAAAATGACAGAGCCGCTTTGACAGATTGTT 801  
 DB 721 CATTAATTCGCTGCGAGATTTTGAAGAAAAATGACAGAGCCGCTTTGACAGATTGTT 780  
 QY 802 TCTAAATCTTAAATTCGCGGCTTATGACAGAAAGCCACAGACATACAGTGAAGATGAA 861  
 DB 781 TCTAAATCTTAAATTCGCGGCTTATGACAGAAAGCCACAGACATACAGTGAAGATGAA 840  
 QY 862 GTACAGAGGTTTAAACAAAAATTAATCTCAAGAGAACCAAAATTAATGAGAGATGCC 921  
 DB 841 GTACAGAGGTTTAAACAAAAATTAATCTCAAGAGAACCAAAATTAATGAGAGATGCC 900  
 QY 922 AATAGCCCAACAGCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 981  
 DB 901 AATAGCCCAACAGCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 960  
 QY 982 ATGCACACCAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1041

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Db      961 ATGGCAGCAATTCMAATGCTCTTCTAAGGAGAGAAAGATGAACAGATCTATACACA 1020
QY      1042 TTAACTTGACAAATGGCTTGGAGAGAGAACTAAACCTACAGTAAACAACTTAG 1101
Db      1021 TTAACTTGACAAATGGCTTGGAGAGAGAACTAAACCTACAGTAAACAACTTAG 1080
QY      1102 GACTTCCAAATATTTCCCAAAATTTCTATGCGCTACTGAAAAAGTATTGATTCAGAAAAAGAA 1161
Db      1081 GAACCTCCAAATATTTCCCAAAATTTCTATGCGCTACTGAAAAAGTATTGATTCAGAAAAAGAA 1140
QY      1162 GCAAAAGAGAAAGAAACACTGATTAATCATGAAACACTATGACTTTGTGAAGATG 1221
Db      1141 GCAAAAGAGAAAGAAACACTGATTAATCATGAAACACTATGACTTTGTGAAGATG 1200
QY      1222 ATGGTGAATATGGAACATATCTCCAGAGAGAGTGTCTTCTACTCTGAAACCTTGAT 1281
Db      1201 ATGGTGAATATGGAACATATCTCCAGAGAGAGTGTCTTCTACTCTGAAACCTTGAT 1260
QY      1282 GAAATGATGCTCTTCCAGACCAAAACAAAGCTAGAAAAAAATGCTACTGACAAATTAAGC 1341
Db      1261 GAAATGATGCTCTTCCAGACCAAAACAAAGCTAGAAAAAAATGCTACTGACAAATTAAGC 1320
QY      1342 AAGCTTTTCCAGACCAATGAGAGAGATGATGAAGAAACAGACAGATACCAAGAGAA 1401
Db      1321 AAGCTTTTCCAGACCAATGAGAGAGATGATGAAGAAACAGACAGATACCAAGAGAA 1380
QY      1402 GCAGCTAAGATGAAAAAGAAATATGGAAGCTTGAAGATTCACAAAAGATGATTAAGC 1461
Db      1381 GCAGCTAAGATGAAAAAGAAATATGGAAGCTTGAAGATTCACAAAAGATGATTAAGC 1440
QY      1462 AACCCAGAGAGAAAGACAGATGAACCCAAAGAAAAACAGAAAGCTATTTGGAAGCCATC 1521
Db      1441 AACCCAGAGAGAAAGACAGATGAACCCAAAGAAAAACAGAAAGCTATTTGGAAGCCATC 1500
QY      1522 AGAAAAATATTTGAATGTTGAAGAAACATGACAAAAAGGAATTAAGAAATTAAGTATGAC 1581
Db      1501 AGAAAAATATTTGAATGTTGAAGAAACATGACAAAAAGGAATTAAGAAATTAAGTATGAC 1560
QY      1582 CTTTCAAGATGAGAGACTTCATCAATTAACAAAGCTGATGCTTATGAGAGAAAGCCATC 1641
Db      1561 CTTTCAAGATGAGAGACTTCATCAATTAACAAAGCTGATGCTTATGAGAGAAAGCCATC 1620
QY      1642 CTTGACAAGAGAAAGCCGAGGCGCATCAAGGCGATTTATGACAGCCCTGTAATAATGCGAA 1701
Db      1621 CTTGACAAGAGAGAAAGCCGAGGCGCATCAAGGCGATTTATGACAGCCCTGTAATAATGCGAA 1680
QY      1702 AAGATCCAGAGAGCTTTCAACTGTTTCAGAAAAACATAATATAGCTTAAACACTTCTAAT 1761
Db      1681 AAGATCCAGAGAGCTTTCAACTGTTTCAGAAAAACATAATATAGCTTAAACACTTCTAAT 1740
QY      1762 TCTGTGATTAATTTTTCACCCAGGTTATTAAGAAAGTGTGAATTTACAGTAACTTA 1821
Db      1741 TCTGTGATTAATTTTTCACCCAGGTTATTAAGAAAGTGTGAATTTACAGTAACTTA 1800
QY      1822 ACCTTTACAGAGTGTAAACATAGCTTCTCCGTAATAAATCTATGTAAGTAAAGT 1881
Db      1801 ACCTTTACAGAGTGTAAACATAGCTTCTCCGTAATAAATCTATGTAAGTAAAGT 1860
QY      1882 TGTATGTAAGCTGAGA 1897
Db      1861 TGTATGTAAGCTGAGA 1876
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RESULT 7  
ID ACA06116 standard; cDNA; 1893 BP.

AC ACA06116;

DT 02-JUN-2003 (first entry)

DE cDNA encoding human PRO polypeptide #18.

```
XX      Human; PRO polypeptide; secreted and transmembrane protein; cancer;  
KW      non-insulin dependent diabetes mellitus; septic shock; stroke;  
KW      rheumatoid arthritis; graft-versus-host disease; cardiac ischaemia;  
KW      psoriasis; immunosuppressive; antineumatic; antidiabetic;  
KW      cytostatic; immunosuppressive; antineumatic; antidiabetic;  
KW      cerebroprotective; vasotropic; antipsoriatic; antiinflammatory;  
KW      antiasclerotic; gene therapy; gene; ss.  
OS      Homo sapiens.  
PN      US2003008348-A1.  
PD      09-JAN-2003.  
XX      26-DEC-2001; 2001US-0035855.  
XX      14-MAY-1999; 99WO-US10733.  
XX      02-DEC-1999; 99WO-US28551.  
XX      22-DEC-1999; 99WO-US30720.  
XX      01-MAR-2000; 2000WO-US05601.  
XX      02-MAR-2000; 2000WO-US05601.  
XX      22-MAY-2000; 2000WO-US05841.  
XX      02-JUN-2000; 2000WO-US14042.  
XX      23-AUG-2000; 2000WO-US15264.  
XX      24-AUG-2000; 2000WO-US23322.  
XX      01-DEC-2000; 2000WO-US32678.  
XX      01-JUN-2001; 2001WO-US17800.  
XX      20-JUN-2001; 2001WO-US19692.  
XX      29-JUN-2001; 2001WO-US21066.  
XX      09-JUL-2001; 2001WO-US21735.  
XX      15-MAY-1998; 98US-085579P.  
XX      15-DEC-1998; 98US-112514P.  
XX      22-DEC-1998; 98US-113300P.  
XX      23-DEC-1998; 98US-113430P.  
XX      23-DEC-1998; 98US-113605P.  
XX      22-JAN-1999; 99US-116843P.  
XX      23-MAR-1999; 99US-125774P.  
XX      23-MAR-1999; 99US-125778P.  
XX      24-MAR-1999; 99US-125826P.  
XX      05-APR-1999; 99US-127035P.  
XX      13-APR-1999; 99US-129122P.  
XX      21-APR-1999; 99US-130359P.  
XX      25-MAY-1999; 99US-135750P.  
XX      08-JUN-1999; 99US-138166P.  
XX      20-JUL-1999; 99US-144791P.  
XX      03-AUG-1999; 99US-146970P.  
XX      29-OCT-1999; 99US-162506P.  
XX      16-AUG-2001; 2001US-0931836.  
XX      (GETH ) GENENTECH INC.  
XX      Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J,  
XX      Stewart TA, Watanabe CK, Wood WJ, Zhang Z;  
XX      WPI; 2003-341326/32.  
XX      P-PsDB; AB069097.  
XX      New PRO polypeptides and nucleic acid molecules, useful for diagnosing  
XX      or treating diabetes mellitus, cancers, septic shock, inflammatory  
XX      or tissue typing  
XX      Claim 2; Fig 35; 196pp; English.  
XX      The present invention relates to the isolation of novel human PRO  
XX      polypeptides, and the polynucleotide sequences encoding them. The  
XX      PRO polypeptides are secreted and transmembrane proteins. The PRO  
XX      polypeptides and polynucleotides are useful in diagnosing or  
XX      treating non-insulin dependent diabetes mellitus, cancers, septic  
XX      shock, rheumatoid arthritis, graft-versus-host disease, stroke, cardiac  
XX      ischaemia, psoriasis, inflammatory bowel disease or asthma. The PRO
```

CC polynucleotide sequences may be used as hybridisation probes in  
CC chromosome and gene mapping, or in generating antisense RNA and DNA.  
CC They are also useful in preparing PRO polypeptides, in assays to  
CC identify other proteins or molecules involved in binding reaction, to  
CC generate transgenic animals or knockout animals, which in turn are  
CC useful in the development and screening of therapeutically useful  
CC reagents, for chromosome identification, and tissue typing. The PRO  
CC polypeptides and nucleic acid molecules are also useful in gene  
CC therapy, and as molecular weight markers for protein electrophoresis  
CC purposes. Anti-PRO antibodies may be used in diagnostic assays for  
CC PRO polypeptides, or for the affinity purification of the polypeptides  
CC from recombinant cell culture or natural sources. The present sequence  
CC represents a cDNA encoding a human PRO polypeptide of the invention.  
xx

SQ Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other:

Query Match 92.5%; Score 1866.4; DB 25; Length 1893;  
Best Local Similarity 99.7%; Pred. No. 0;

Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 22 GTCTCCGGCTACAGAACTTACAGACCCACAGGGGAGACAGCGCTCCCTCTACTGGA 81
DB 1 GTCTCCGGCTACAGAACTTACAGACCCACAGGGGAGACAGCGCTCCCTCTACTGGA 60
QY 82 GACTTGACTCCGGGGGCGCCCAACCGCTTATCCCTGACCGCTGAGTGCAGATCC 141
DB 61 GACTTGACTCCGGGGGCGCCCAACCGCTTATCCCTGACCGCTGAGTGCAGATCC 120
QY 142 TGCAGCCGCCAGTCCCGGCCCTCTCCGGCCCAACCCACCTCTGCGCTCTCTCTGT 201
DB 121 TGCAGCCGCCAGTCCCGGCCCTCTCCGGCCCAACCCACCTCTGCGCTCTCTCTGT 180
QY 202 TTTTACTCTCTCTTTTCACTTATTAACAAGCTACAGTCCAGAGCCCGCGGCGCT 261
DB 181 TTTTACTCTCTCTTTTCACTTATTAACAAGCTACAGTCCAGAGCCCGCGGCGCT 240
QY 262 GTGACCCCAAGCGAGCGTGAAGAATGGGTTTCCCGGGACCGGACTTGATTTGGTG 321
DB 241 GTGACCCCAAGCGAGCGTGAAGAATGGGTTTCCCGGGACCGGACTTGATTTGGTG 300
QY 322 TTAAGTCTCCGATTCAGAGCTTTTCCCAACCTGAGAGAGCCAAAGATCTCTACAT 381
DB 301 TTAAGTCTCCGATTCAGAGCTTTTCCCAACCTGAGAGAGCCAAAGATCTCTACAT 360
QY 382 AATAGAGATTAATAGTGCAGAAAGACCTTTGAATGATGATGCTGTAAGCAGAGAGAC 441
DB 361 AATAGAGATTAATAGTGCAGAAAGACCTTTGAATGATGATGCTGTAAGCAGAGAGAC 420
QY 442 AAGATTAAAAAACAATATCTCTCCAGAAAAACAAGCGTCAAGAGCACTATTCTTGT 501
DB 421 AAGATTAAAAAACAATATCTCTCCAGAAAAACAAGCGTCAAGAGCACTATTCTTGT 480
QY 502 GATAACTTGAACCTGCTAAGGGCAATTAACAGAAAAAGAAAAATTGAGAAAGAAAGACA 561
DB 481 GATAACTTGAACCTGCTAAGGGCAATTAACAGAAAAAGAAAAATTGAGAAAGAAAGACA 540
QY 562 TCTATTAACAAGCTCCCACTTGATTAATTAAGTTGAATGGAAGATGTTGATTAACCAAG 621
DB 541 TCTATTAACAAGCTCCCACTTGATTAATTAAGTTGAATGGAAGATGTTGATTAACCAAG 600
QY 622 AATGCAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 681
DB 601 AATGCAAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 682 GATGATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 741
DB 661 GATGATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 742 CATAAATCGTGCAGAGATTTATGAGAAAAATGACAGAGCCGTGTTGACAGATTTGT 801
DB 721 CATAAATCGTGCAGAGATTTATGAGAAAAATGACAGAGCCGTGTTGACAGATTTGT 780
QY 802 TCTAAACTACTTAATCTCGGCTTATCAAGAAACCAAGCAATACACTGGAAGATGA 861
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DB 781 TCTAAACTACTTAATCTCGGCTTATCAAGAAACCAAGCAATACACTGGAAGATGA 840
QY 862 GTAGCAGAGGTTTTCACAAAAATTAATCTCAAAAGAGCCAAACAAATTAAGAGAGATCCC 921
DB 841 GTAGCAGAGGTTTTCACAAAAATTAATCTCAAAAGAGCCAAACAAATTAAGAGAGATCCC 900
QY 922 AATAAGCCCAAGCTGACATGAGATATAGCTGGAATAATTCAGAGAAAGTCACTCA 981
DB 901 AATAAGCCCAAGCTGACATGAGATATAGCTGGAATAATTCAGAGAAAGTCACTCA 960
QY 982 ATGGCAGCAATTCAGATGCTTCTTAAGGAGAGAAAGATGAAGACGTATCTAACACA 1041
DB 961 ATGGCAGCAATTCAGATGCTTCTTAAGGAGAGAAAGATGAAGACGTATCTAACACA 1020
QY 1042 TTAACCTTGACAAATGCTTGGAAGAGAACTAAACCTACAGTGAAGACACTTTAGG 1101
DB 1021 TTAACCTTGACAAATGCTTGGAAGAGAACTAAACCTACAGTGAAGACACTTTAGG 1080
QY 1102 GACTTCCAAATTTTCCCAATTTTCTATCGCTACTGAAAGATTTGATTCAGAAAAAGAA 1161
DB 1081 GAACCTCAATATTTTCCCAATTTTCTATCGCTACTGAAAGATTTGATTCAGAAAAAGAA 1140
QY 1162 GCAAAAGAGAAAGAAAGAACTGATTTCTATCATGAAAGAACTGATTTGATTTGAGATG 1221
DB 1141 GCAAAAGAGAAAGAAAGAACTGATTTCTATCATGAAAGAACTGATTTGATTTGAGATG 1200
QY 1222 ATGGTAATATGAAACATATCTCCAGAAAGAGTGTTCCTACCTTGAAACCTTGAT 1281
DB 1201 ATGGTAATATGAAACATATCTCCAGAAAGAGTGTTCCTACCTTGAAACCTTGAT 1260
QY 1282 GAATGATTTGCTTTTCAACACCAAAACAAAGCTAGAAAAAATGCTACTGACAAATTAAGC 1341
DB 1261 GAATGATTTGCTTTTCAACACCAAAACAAAGCTAGAAAAAATGCTACTGACAAATTAAGC 1320
QY 1342 AAGCTTTTCCAGAGCCATCAGAGAGAGAGTCAATGAAGAAACAGACAGTACCAAGAGAA 1401
DB 1321 AAGCTTTTCCAGAGCCATCAGAGAGAGAGTCAATGAAGAAACAGACAGTACCAAGAGAA 1380
QY 1402 GCAGCTAAGATGAAAGAAATATGGAAGCTTGAAGATTCACAAAAGATGATTAATCTCC 1461
DB 1381 GCAGCTAAGATGAAAGAAATATGGAAGCTTGAAGATTCACAAAAGATGATTAATCTCC 1440
QY 1462 AACCCAGAGAGAGAGAGAGATGAAACCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1521
DB 1441 AACCCAGAGAGAGAGAGAGATGAAACCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1522 AGAAAAAATATTTGAATGCTTGAAGAAACATGCAAAAAAGGAAATTAAGAGATTAAGC 1581
DB 1501 AGAAAAAATATTTGAATGCTTGAAGAAACATGCAAAAAAGGAAATTAAGAGATTAAGC 1560
QY 1582 CTTTCAAGATGAGAGACTTCAATTAACAGCTGATGCTTATGAGAGAAAGGCATC 1641
DB 1561 CTTTCAAGATGAGAGACTTCAATTAACAGCTGATGCTTATGAGAGAAAGGCATC 1620
QY 1642 CTTGACAGAGAAAGCCGAGGCTTCAAGGCGATTTTATGACAGCCTTAATAAATGCGAA 1701
DB 1621 CTTGACAGAGAAAGCCGAGGCTTCAAGGCGATTTTATGACAGCCTTAATAAATGCGAA 1680
QY 1702 AAGATCCAGAGATCTTTCAACGTTTCAAGAAACATTAATTAAGCTTAATAAAGCTTCAAT 1761
DB 1681 AAGATCCAGAGATCTTTCAACGTTTCAAGAAACATTAATTAAGCTTAATAAAGCTTCAAT 1740
QY 1762 TCTGTATTAATAATTTTGAAGCCCAAGGTTATTAAGAAAGTGTGAATTTACAGTAGTTA 1821
DB 1741 TCTGTATTAATAATTTTGAAGCCCAAGGTTATTAAGAAAGTGTGAATTTACAGTAGTTA 1800
QY 1822 ACCTTTTCAAGTGTATTAACATATGCTTTTCCCGTAAAAACATATCTGAAAGTAAGT 1881
DB 1801 ACCTTTTCAAGTGTATTAACATATGCTTTTCCCGTAAAAACATATCTGAAAGTAAGT 1860
QY 1882 TGTATTAAGCTGAGA 1897
DB 1861 TGTATTAAGCTGAGA 1840
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Db 1861 TGTATGTAAGCTGAAA 1876

RESULT 8  
ACAO6173  
ID ACA06173 standard; cDNA; 1893 BP.  
XX  
XX ACA06173;  
AC  
XX  
XX 02-JUN-2003 (first entry)  
DT  
XX  
XX CDNA encoding human PRO polypeptide #18.  
DE  
XX  
XX Human; secreted and transmembrane protein; bone disorder; obesity;  
KW cartilage disorder; sports injury; arthritis; diabetes mellitus;  
KW hypo-insulinaemia; obesity; hyper-insulinaemia; thalassaemia;  
KW haemoglobin-associated disorder; kidney disorder; Berger disease;  
KW mesangial cell function; nephropathy; Schonlein-Henoch purpura;  
KW celiac disease; dermatitis herpetiformis; Crohn's disease;  
KW anorectic; antiarthritic; antidiabetic; antianemic; nephrotoxic;  
KW antiinflammatory; gene therapy; gene; ss.  
OS  
XX Homo sapiens.  
XX  
XX US2003032061-A1.  
XX  
XX 13-FEB-2003.  
XX  
XX 26-DEC-2001; 2001US-0036214.  
XX  
XX 14-MAY-1999; 99WO-US10733.  
PR 02-DEC-1999; 99WO-US28551.  
PR 22-DEC-1999; 99WO-US30720.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US14042.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 23-AUG-2000; 2000WO-US33522.  
PR 24-AUG-2000; 2000WO-US33328.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 15-MAY-1998; 98US-085579P.  
PR 15-DEC-1998; 98US-112514P.  
PR 22-DEC-1998; 98US-113300P.  
PR 23-DEC-1998; 98US-113430P.  
PR 23-DEC-1998; 98US-113605P.  
PR 23-DEC-1998; 98US-113621P.  
PR 23-DEC-1998; 98US-114140P.  
PR 12-JAN-1999; 99US-115552P.  
PR 22-JAN-1999; 99US-116843P.  
PR 23-MAR-1999; 99US-125774P.  
PR 23-MAR-1999; 99US-125778P.  
PR 24-MAR-1999; 99US-125826P.  
PR 31-MAR-1999; 99US-127035P.  
PR 03-APR-1999; 99US-127706P.  
PR 13-APR-1999; 99US-129122P.  
PR 21-APR-1999; 99US-130359P.  
PR 27-APR-1999; 99US-131270P.  
PR 27-APR-1999; 99US-131272P.  
PR 27-APR-1999; 99US-131291P.  
PR 04-MAY-1999; 99US-132371P.  
PR 04-MAY-1999; 99US-132379P.  
PR 04-MAY-1999; 99US-132383P.  
PR 25-MAY-1999; 99US-135750P.  
PR 08-JUN-1999; 99US-138156P.  
PR 20-JUL-1999; 99US-144791P.  
PR 03-AUG-1999; 99US-146970P.  
PR 29-OCT-1999; 99US-162506P.

PR 16-AUG-2001; 2001US-0931836.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J,  
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX WPI: 2003-341962/32.  
DR  
DR P-PSDB; AB069120.  
XX  
XX  
PT Novel isolated PRO polypeptides e.g., PRO4334, PRO1122, PRO1889,  
PT PRO1890, PRO1887, PRO1785, PRO4353, useful for treating sports  
PT injuries, arthritis, diabetes, obesity, hyper- or hypo-insulinaemia -  
XX  
XX Claim 2; Fig 35; 194pp; English.  
XX  
XX The present invention relates to the isolation of novel human PRO  
XX polypeptides, and the polynucleotide sequences encoding them. The  
XX PRO polypeptides are secreted and transmembrane proteins. The PRO  
XX polypeptides and polynucleotides are useful in diagnosing or  
XX treating various bone and/or cartilage disorders (e.g. sports  
XX injuries, arthritis), various insulin deficient states (e.g. diabetes  
XX mellitus, hypo-insulinaemia), obesity, hyper-insulinaemia,  
XX haemoglobin-associated disorders (e.g. thalassaemias), kidney disorders  
XX or other nephropathies associated with Schonlein-Henoch purpura,  
XX celiac disease, dermatitis herpetiformis or Crohn's disease. The PRO  
XX polynucleotide sequences may be used as hybridisation probes in  
XX chromosome and gene mapping, or in generating antisense RNA and DNA.  
XX They are also useful in preparing PRO polypeptides, in assays to  
XX identify other proteins or molecules involved in binding reaction, to  
XX generate transgenic animals or knockout animals, which in turn are  
XX useful in the development and screening of therapeutically useful  
XX reagents, for chromosome identification, and tissue typing. The PRO  
XX polypeptides and nucleic acid molecules are also useful in gene  
XX therapy, and as molecular weight markers for protein electrophoresis  
XX purposes. Anti-PRO antibodies may be used in diagnostic assays for  
XX PRO polypeptides, or for the affinity purification of the polypeptides  
XX from recombinant cell culture or natural sources. The present sequence  
XX represents a cDNA encoding a human PRO polypeptide of the invention.  
SQ  
Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other;  
Query Match 92.5%; Score 1866.4; DB 25; Length 1893;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 22 GTCTCCGCGTACAGAACTTCAGACCCACAGAGGGGAGAGGCTCCCTTACCTGGA 81  
DB 1 GTCTCCGCGTACAGAACTTCAGACCCACAGAGGGGAGAGGCTCCCTTACCTGGA 60  
QY 82 GACTTACATCCCGCGGGGGCCCAACCTGCTATCCCTTACCGTGCAGTGTAGAGATCC 141  
DB 61 GACTTACATCCCGCGGGGGCCCAACCTGCTATCCCTTACCGTGCAGTGTAGAGATCC 120  
QY 142 TGCAGCGCGCCAGTCCCGGCCCTCTCCGCCCCACACCCACCTCTCTGCTCTGCT 201  
DB 121 TGCAGCGCGCCAGTCCCGGCCCTCTCTCCGCCCCACACCCACCTCTCTGCTCTGCT 180  
QY 202 TTTTACTCTCTCTTTTCAATTAACAAAGCTACAGCTCCAGAGGCCAGCGCGGCT 261  
DB 181 TTTTACTCTCTCTTTTCAATTAACAAAGCTACAGCTCCAGAGGCCAGCGCGGCT 240  
QY 262 GTGACCCAGCGGAGCGTGAAGAAAGGCTTCTCGGAGCCGAGCTTGTGCTG 321  
DB 241 GTGACCCAGCGGAGCGTGAAGAAAGGCTTCTCGGAGCCGAGCTTGTGCTG 300  
QY 322 TTAGTGTCTCCGATTCAGCTTCCCAAACTGGAGAGGCAAGCAAAATCTCTACAT 381  
DB 301 TTAGTGTCTCCGATTCAGCTTCCCAAACTGGAGAGGCAAGCAAAATCTCTACAT 360  
QY 382 AATAGAGATTAAAGTCAGAAAGACTTTGAATGACAGATTGCTGAAGCAGAGAGAC 441



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Db 361 AATAGAGATTAACTGACAGAAAGACCTTTGATGACAGATTGCTGAAGCAGCAAGAAAGAC 420
QY 442 AAGATTAATAAATAACATATCTCCAGAAAACAAGCCAGCTCAGACGACTATTTCTTTGTT 501
Db 421 AAGATTAAAAAATATCTCCAGAAAACAAGCCAGCTCAGACGACTATTTCTTTGTT 480
QY 502 GATACTGTAACCTGCTTAAGGCAATTAACAGAAAAGAAAAAATTGACAGAAAGAACAA 561
Db 481 GATTAACCTGTAACCTGCTTAAGGCAATTAACAGAAAAGAAAAAATTGACAGAAAGAACAA 540
QY 552 TCTATTAAGAGCTCCCACTTGATTAATAAGTTGATGGAAGATGTTGATTTCAACCAAG 621
Db 541 TCTATTAAGAGCTCCCACTTGATTAATAAGTTGATGGAAGATGTTGATTTCAACCAAG 600
QY 622 AATGAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 681
Db 601 AATGAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 682 GATGATCCAGATGCTTCATCACTAGACGGGACTCCTTTAACCCGCTGAAGACATTTGTC 741
Db 661 GATGATCCAGATGCTTCATCACTAGACGGGACTCCTTTAACCCGCTGAAGACATTTGTC 720
QY 742 CATAAATGCTGCGCAGGATTTATGAGAAAATGACAGAGCCGTTGTTGACAAAGATTGTT 801
Db 721 CATAAATGCTGCGCAGGATTTATGAGAAAATGACAGAGCCGTTGTTGACAAAGATTGTT 780
QY 802 TCTAACTACTTATCTGCGCTTATCAAGAAAAGCCAGACATACCTGAGAGATGAA 861
Db 781 TCTAACTACTTATCTGCGCTTATCAAGAAAAGCCAGACATACCTGAGAGATGAA 840
QY 862 GTAGCAGAGGTTTTCAAAATTTAATCTCAAGAGGCAACAATTAAGAGAGATGCC 921
Db 841 GTAGCAGAGGTTTTCAAAATTTAATCTCAAGAGGCAACAATTAAGAGAGATGCC 900
QY 922 AATAAGCCACAGCTGAGCTGAGATCAGGCTGGAATAATACAGAGAAAGTGACTCCA 981
Db 901 AATAAGCCACAGCTGAGCTGAGATCAGGCTGGAATAATACAGAGAAAGTGACTCCA 960
QY 982 ATGGCAGCAATTCAGATGCTGCTTGAAGGAGAAAACGATGAACAGTATCTAACACA 1041
Db 961 ATGGCAGCAATTCAGATGCTGCTTGAAGGAGAAAACGATGAACAGTATCTAACACA 1020
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Db 1021 TTAACCTTGACAAATGGCTTGAAGAGGAACTAAACCTCAGTGAAGACAACTTTAGG 1080
QY 1102 GACTTCCAAATATTTCCAAATTTCTATCGCTACTGAAGAGTATGATTCAGAAAAGAA 1161
Db 1081 GACTTCCAAATATTTCCAAATTTCTATCGCTACTGAAGAGTATGATTCAGAAAAGAA 1140
QY 1162 GCAAAAGAGAAAACACTGATTAATCAATGAAGAACTGATGACTTTGTGAAGATG 1221
Db 1141 GCAAAAGAGAAAACACTGATTAATCAATGAAGAACTGATGACTTTGTGAAGATG 1200
QY 1222 ATGGGAAATATGGAACAATATCTCCAGAAAGGTTTCTTCTTCTTCTTCTTCTTCTTCT 1281
Db 1201 ATGGGAAATATGGAACAATATCTCCAGAAAGGTTTCTTCTTCTTCTTCTTCTTCTTCT 1260
QY 1282 GAAATGATTTGCTTCTCAAGACCAAAAACAAGCTAGAAAATAATGCTAGCAATATTAAGC 1341
Db 1261 GAAATGATTTGCTTCTCAAGACCAAAAACAAGCTAGAAAATAATGCTAGCAATATTAAGC 1320
QY 1342 AAGCTTTTCCAGACCAATCAAGAGAGATCAATGAAGAAAGACAGACAGTACCAAGAGAA 1401
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QY 1402 GCAGCTAAGATGGAAGAAAGATATGGAAGCTTTGCAACAAAAGATGATTAAGTCC 1461
Db 1381 GCAGCTAAGATGGAAGAAAGATATGGAAGCTTTGCAACAAAAGATGATTAAGTCC 1440
QY 1462 AACCAGAGAGAAAGACAGATGAAGCCCAAGAGAAAACAGAAAGCTATTTGGAAGCCATC 1521
Db 1441 AACCAGAGAGAAAGACAGATGAAGCCCAAGAGAAAACAGAAAGCTATTTGGAAGCCATC 1500
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QY 1522 AGAAAAATATTGATGCTTGAGAGAAACATGACAAAAGGAAATTAAGAGATTATGAC 1581
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Db 1561 CTTTCAAGATGAGAGACTTCATCAATTAACAGCTGATGCTTATGAGAGAAAGCATC 1620
QY 1642 CTTGACAGAGAAAGAGCCAGGCCATCAAGCCATTTATAGCAGCCCTGTAATAATGCAA 1701
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Db 1741 TCTGTGATTTAAATTTTGAACCCCAAGGTTATTAAGAAAGCTGATTTACAGTATTA 1800
QY 1822 ACCTTTACAGTGTAAACATAGCTTTCCCGTAAATAATCTGAAAGTAAAGT 1881
Db 1801 ACCTTTACAGTGTAAACATAGCTTTCCCGTAAATAATCTGAAAGTAAAGT 1860
QY 1882 TGTATGTAAGCTGAGA 1897
Db 1861 TGTATGTAAGCTGAGA 1876

RESULT 9
ACA58884
ID ACA58884 standard; cDNA, 1893 BP.
XX
AC ACA58884;
XX
DT 10-JUN-2003 (first entry)
XX
DE cDNA encoding human secreted polypeptide PRO5990.
XX
KW Human; ss; gene; gene therapy; tumour; cancer.
XX
OS Homo sapiens.
XX
PN US2003013855-A1.
XX
PD 16-JAN-2003.
XX
PF 03-MAY-2002; 2002US-0063616.
XX
PR 30-DEC-1998; 98KR-0062142.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 30-DEC-1999; 99WO-US31274.
PR 18-FEB-2000; 2000WO-US04341.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 21-MAR-2000; 2000WO-US07532.
PR 22-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US15264.
PR 24-AUG-2000; 2000WO-US23328.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 14-MAY-1999; 99US-0311832.
PR 25-AUG-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380139.
PR 25-AUG-1999; 99US-0380142.
PR 15-SEP-1999; 99US-0397342.
PR 18-OCT-1999; 99US-0403297.
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PR	12-NOV-1999;	99US-0423844.	
PR	12-AUG-2000;	2000US-0644848.	
PR	18-SEP-2000;	2000US-0664810.	
PR	18-SEP-2000;	2000US-0665350.	
PR	08-NOV-2000;	2000US-0709238.	
PR	20-DEC-2000;	2000US-0747259.	
PR	22-MAR-2001;	2001US-0816744.	
PR	10-MAY-2001;	2001US-0854208.	
PR	10-MAY-2001;	2001US-0854280.	
PR	30-MAY-2001;	2001US-0870574.	
PR	05-JUN-2001;	2001US-0874503.	
PR	29-JUN-2001;	2001US-0869599.	
PR	18-JUL-2001;	2001US-0908827.	
PR	06-DEC-2001;	2001US-0006867.	
XX			
XA	(GETH )	GENENTECH INC.	
XA			
PI	Eaton DL, Flivaroff E, Gerritsen ME, Goddard A, Godowski PJ,		
PI	Grimaldi JC, Gurney AL, Watanabe CK, Wood WI,		
XX			
DR	WPI: 2003-330485/31.		
XX	P-SDB; AB071580.		
PT	New isolated antibody specifically binding a PRO polypeptide, useful		
PT	for the preparation of a medicament for treating disorders with the		
PT	aberrant expression or activity of the PRO polypeptide, such as tumor		
PT	conditions and cancer		
XX			
PS	Example 4; Page 217-218; 406pp; English.		
XX			
CC	The invention relates to an antibody that binds to a polypeptide with a		
CC	fully defined sequence given in the specification. The methods and		
CC	compositions (containing antibodies that specifically bind a PRO		
CC	polypeptide) of the present invention are useful for the preparation of a		
CC	medicament for the treatment of disorders associated with the aberrant		
CC	expression or activity of the PRO polypeptide, such as tumour conditions		
CC	and cancer. They can also be used to generate transgenic or knockout		
CC	animals useful in the development and screening of therapeutically useful		
CC	reagents. The PRO polypeptides and encoding nucleic acids can be used as		
CC	molecular weight markers for protein electrophoresis, chromosome		
CC	identification and tissue typing. The PRO polypeptides are useful to		
CC	induce angiogenesis e.g wound healing. The PRO polypeptides are useful to		
CC	joint problems, articular cartilage defects, osteoarthritis or rheumatoid		
CC	arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The		
CC	antibodies may be used in various diagnostic, competitive binding and/or		
CC	immunoprecipitation assays. The present sequence represents a cDNA		
CC	encoding a PRO polypeptide of the invention.		
XX			
SO	Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other;		
Query Match	92.5%; Score 1866.4; DB 25; Length 1893;		
Best Local Similarity	99.7%; Pred. No. 0;		
Matches 1870; Conservative	0; Mismatches 6; Indels 0; Gaps 0		
QY	22 GTCTCCGGGTACAGAACTTCAGACACCACAGGGCGAGACGCTCCCTCTACCTGGA	81	
Db	1 GTCTCCGGGTACAGAACTTCAGACACCACAGGGCGAGACGCTCCCTCTACTGGA	60	
QY	82 GACTTGATATCCCGCGCGGCCCAACCTGCTATTCCTTGACCGTGAAGTGCAGATCC	141	
Db	61 GACTTGATATCCCGCGCGGCCCAACCTGCTATTCCTTGACCGTGAAGTGCAGATCC	120	
QY	142 TGCAGCGCCACAGTCCCGGCCCTCTCCCGCCACACACACCCCTCGGGCTCTTCGCT	201	
Db	121 TGCAGCGCCACAGTCCCGGCCCTCTCCCGCCACACACACCTCTCTGCTCTTCGCT	180	
QY	202 TTTTACTCTCTCTTTTCATTATACAAAGACTACAGCTCCAGAGACCCAGCGCGGCT	261	
Db	181 TTTTACTCTCTCTTTTCATTATACAAAGACTACAGCTCCAGAGACCCAGCGCGGCT	240	
QY	262 GTGACCCCAAGCGAGCGTGAAGATGGGGTTCCTCGGGACCGGACTTGGATTGTGGTG	321	
Db	241 GTGACCCCAAGCGAGCGTGAAGATGGGGTTCCTCGGGACCGGACTTGGATTGTGGTG	300	

QY	322	TTAAGTCCCGGATTCAACGTTTCCCAAAACCTGAGAGAAAGCCAAATCTTACAT	381
Db	301	TTATGTCTCCCGATTCAAGCTTTCCCAAAACCTGAGAGAAAGCCAAATCTTACAT	360
QY	382	AATGAGAAATTAAGTGCAGAGAAAGACCTTTGAATGAAGACAGATTTCTGAGAGAGAAAGAC	441
Db	361	AATGAGAAATTAAGTGCAGAGAAAGACCTTTGAATGAAGACAGATTTCTGAGAGAGAAAGAC	420
QY	442	AAGTTTAAAAAAACATATCTCTCCAGAAAGAACCCAGCTCAGAGCAATATCTTTGTT	501
Db	421	AAGTTTAAAAAAACATATCTCTCCAGAAAGAACCCAGCTCAGAGCAATATCTTTGTT	480
QY	502	GATTAACCTTGAACCTGGCTAAGGGCAATTAACGAAAGAAAGAAAAATTTGAGAAAGAAACACA	561
Db	481	GATTAACCTTGAACCTGGCTAAGGGCAATTAACGAAAGAAAGAAAAATTTGAGAAAGAAACACA	540
QY	562	TCTATAGAAGAGCTCCCACTTGATTAATGAATTGAATGTGGAAAGATGTGATTCACACAG	621
Db	541	TCTATAGAAGAGCTCCCACTTGATTAATGAATTGAATGTGGAAAGATGTGATTCACACAG	600
QY	622	AATCGAAAATCGATGCATGATTTATGACTTACTTAAGATGTGATTCATTAATTTCAA	681
Db	601	AATCGAAAATCGATGCATGATTTATGACTTACTTAAGATGTGATTCATTAATTTCAA	660
QY	682	GATGATTCAGATGTGCTTCATCAACAGAGAGGAGCTCTTAACCGCTCAGACATTTGC	741
Db	661	GATGATTCAGATGTGCTTCATCAACAGAGAGGAGCTCTTAACCGCTCAGACATTTGC	720
QY	742	CATTAATAATGGCTGCCAGGATTTATGAAGAAATGACAGAGCCGTGTTGACAAGATTGTT	801
Db	721	CATTAATAATGGCTGCCAGGATTTATGAAGAAATGACAGAGCCGTGTTGACAAGATTGTT	780
QY	802	TCTAAACTACTTAATCTCGGCTTATACAGAGAAAGCAACGACATTAACCTGGAAGATGAA	861
Db	781	TCTAAACTACTTAATCTCGGCTTATACAGAGAAAGCAACGACATTAACCTGGAAGATGAA	840
QY	862	GTAGCAGAGGTTTACAAAATTTAATCTCAGAAAGAACCAATTTATGAGAGGATCCC	921
Db	841	GTAGCAGAGGTTTACAAAATTTAATCTCAGAAAGAACCAATTTATGAGAGGATCCC	900
QY	922	AATTAAGCCCAACAAGCTGGAGCTGAGAAATCAGCGTGGAAAAATTTCCAGAGAAAGTGACTCCA	981
Db	901	AATTAAGCCCAACAAGCTGGAGCTGAGAAATCAGCGTGGAAAAATTTCCAGAGAAAGTGACTCCA	960
QY	982	ATGCGAGCAATTCAGATGTGCTTCTTAAGGGAGAAACGATGAACAGTATCTTAACACA	1041
Db	961	ATGCGAGCAATTCAGATGTGCTTCTTAAGGGAGAAACGATGAACAGTATCTTAACACA	1020
QY	1042	TTAACCCTTGACAAATGGCTTGGAAAGGAACTTAACCTACAGTGAAGACACTTTAGG	1101
Db	1021	TTAACCCTTGACAAATGGCTTGGAAAGGAACTTAACCTACAGTGAAGACACTTTAGG	1080
QY	1102	GACTTCCCAATATTTTCCCAAAATTTCTATCGCTACAGAAAGCATTTATGATTGAGAAAAAGAA	1161
Db	1081	GACTTCCCAATATTTTCCCAAAATTTCTATCGCTACAGAAAGCATTTATGATTGAGAAAAAGAA	1140
QY	1162	GCAAAAAGGAAAGAAACACTGATTAATCTATCATGAAGAACCTGATTGACTTTGTGAAGATG	1221
Db	1141	GCAAAAAGGAAAGAAACACTGATTAATCTATCATGAAGAACCTGATTGACTTTGTGAAGATG	1200
QY	1222	ATGCGAATATATGGAACAATATCTCCAGAAACAAGAGTTCCTACCTTTGAAAACTTGAT	1281
Db	1201	ATGCGAATATATGGAACAATATCTCCAGAAACAAGAGTTCCTACCTTTGAAAACTTGAT	1260
QY	1282	GAAATGATGTGCTCTTCAGACCAACCAAGCTAGAAAAAAATGCTACTGCAATATATAGC	1341
Db	1261	GAAATGATGTGCTCTTCAGACCAACCAAGCTAGAAAAAAATGCTACTGCAATATATAGC	1320
QY	1342	AAGCTTTTCCAGACCATCAGAGAAAGTCTATGAAGAACAGACAGTACCAAGGAAGAA	1401
Db	1321	AAGCTTTTCCAGACCATCAGAGAAAGTCTATGAAGAACAGACAGTACCAAGGAAGAA	1380

QY 1402 GCACCTAAGATGAAAGAAATATGAGAGCTTGAAGATTCACAAAAGATGATACCTC 1461  
 DB 1381 GCACCTAAGATGAAAGAAATATGAGAGCTTGAAGATTCACAAAAGATGATACCTC 1440  
 QY 1462 AACCCAGAGGAGAAAGACAGATGAACCCAAAGAAAAACAGAGCCATTTTGGAAAGCCATC 1521  
 DB 1441 AACCCAGAGGAGAAAGACAGATGAACCCAAAGAAAAACAGAGCCATTTTGGAAAGCCATC 1500  
 QY 1522 AGAAAAAATATGAAATGTTGAAAGAAACATACAAAAGGAAATTAAGAAATATATAC 1581  
 DB 1501 AGAAAAAATATGAAATGTTGAAAGAAACATACAAAAGGAAATTAAGAAATATATAC 1560  
 QY 1582 CTTTCAAGATGAGAGAGCTTCATCAATTAACAGCTGATGCTTATGTGAGAAAGCCATC 1641  
 DB 1561 CTTTCAAGATGAGAGAGCTTCATCAATTAACAGCTGATGCTTATGTGAGAAAGCCATC 1620  
 QY 1642 CTTGACAAGAAAGAGCCGAGCCATCAAGCCATTTATAGACGCTGTAAATAATGCGAA 1701  
 DB 1621 CTTGACAAGAAAGAGCCGAGCCATCAAGCCATTTATAGACGCTGTAAATAATGCGAA 1680  
 QY 1702 AAGATCCAGAGAGCTTTTCACTGTTTCAGAAAAATATATAGCTTAAACACTTCTAT 1761  
 DB 1681 AAGATCCAGAGAGCTTTTCACTGTTTCAGAAAAATATATAGCTTAAACACTTCTAT 1740  
 QY 1762 TCTGTGATTAATTTTGTGACCCAGAGGCTTATAGAAAGTGTGAATTTACAGTAGT 1821  
 DB 1741 TCTGTGATTAATTTTGTGACCCAGAGGCTTATAGAAAGTGTGAATTTACAGTAGT 1800  
 QY 1822 ACCTTTAAAGAGGTTTAAACATATAGCTTTTCCCGTAAATAACTATCTGAAGTAAAGT 1881  
 DB 1801 ACCTTTAAAGAGGTTTAAACATATAGCTTTTCCCGTAAATAACTATCTGAAGTAAAGT 1860  
 QY 1882 TGTATGTAGCTGAGA 1897  
 DB 1861 TGTATGTAGCTGAGA 1876

RESULT 10  
 ID ACA60437 standard; cDNA; 1893 BP.  
 AC ACA60437;  
 XX 11-JUN-2003 (first entry)  
 DE Novel human secreted and transmembrane protein PRO5990 cDNA.  
 KW Human; secreted and transmembrane polypeptide; gene; ss.  
 KW Chromosome mapping; gene mapping; transgenic animal; knockout animal;  
 KW therapeutic agent screening; chromosome identification; tissue typing;  
 KW gene therapy.  
 OS Homo sapiens.  
 PN US2003018183-A1.  
 XX 23-JAN-2003.  
 XX 01-MAY-2002; 2002US-0063512.  
 XX 06-DEC-2001; 2001US-0006867.  
 PA (GETH ) GENENTECH INC.  
 PI Eaton DL, Filvaroff E, Gerlitsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 DR WPI: 2003-330984/31.  
 DR P-PSDB; AB072026.  
 PT New secreted and transmembrane PRO polypeptides and nucleic acid  
 PT molecules encoding the polypeptides, useful in gene therapy or  
 PT preparing a medicament for treating a condition that is responsive to

PT the PRO polypeptide or antibody  
 XX Disclosure: Fig 149; 409pp; English.  
 XX  
 CC The invention describes novel isolated PRO polypeptides. The PRO  
 CC polypeptides or anti-PRO antibodies are useful in preparing a medicament  
 CC for treating a condition that is responsive to the PRO polypeptide or  
 CC antibody. The PRO nucleotide sequences may be used as hybridisation  
 CC probes in chromosome and gene mapping, or in generating antisense RNA  
 CC and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,  
 CC in assays to identify other proteins or molecules involved in binding  
 CC reaction, to generate transgenic animals or knockout animals, which in  
 CC turn are useful in the development and screening of therapeutically  
 CC useful reagents, for chromosome identification, and tissue typing. The  
 CC PRO polypeptides and nucleic acid molecules are also useful in gene  
 CC therapy, and as molecular weight markers for protein electrophoresis  
 CC purposes. The anti-PRO antibodies may be used in diagnostic assays for  
 CC PRO, or for the affinity purification of PRO from recombinant cell  
 CC culture or natural sources. This sequence encodes a novel human  
 CC secreted and transmembrane PRO polypeptide.  
 SQ Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other:  
 Query Match 92.5%; Score 1866.4; DB 25; Length 1893;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 22 GTCTCCGGTCACAGAACTTACAGCCACAGAGGCGAGACGCTCCCTTACCTGGA 81  
 DB 1 GTCTCCGGTCACAGAACTTACAGCCACAGAGGCGAGACGCTCCCTTACCTGGA 60  
 QY 82 GACTTGATCCCGGCGGCGCCCAACCTCTTATATCCTTGACCGCTGAGATGACAGATCC 141  
 DB 61 GACTTGATCCCGGCGGCGCCCAACCTCTTATATCCTTGACCGCTGAGATGACAGATCC 120  
 QY 142 TGCAGCCGCGAGTCCGCGGCGCTCTCCGCGCCACAGCCACCTCTGCGCTCTCTCTGT 201  
 DB 121 TGCAGCCGCGAGTCCGCGGCGCTCTCCGCGCCACAGCCACCTCTGCGCTCTCTCTGT 180  
 QY 202 TTTTACTCTCTCTTTCATTCATTAACAAGCTACAGCTCAGAGAGCCAGCGCGGCT 261  
 DB 181 TTTTACTCTCTCTTTCATTCATTAACAAGCTACAGCTCAGAGAGCCAGCGCGGCT 240  
 QY 262 GTGACCCAGAGCGAGCTGGAAGAAATGGGGTTCTCCGGGACCGGCACTTGGATTCGTG 321  
 DB 241 GTGACCCAGAGCGAGCTGGAAGAAATGGGGTTCTCCGGGACCGGCACTTGGATTCGTG 300  
 QY 322 TTAGGCTCCGATTCAGAGCTTTCCCAACCTGGAGAGCAAGACAAATCTTACAT 381  
 DB 301 TTAGGCTCCGATTCAGAGCTTTCCCAACCTGGAGAGCAAGACAAATCTTACAT 360  
 QY 382 AATAGAGATTAAGTGCAGAAAGACCTTGAATGAACAGATGCTGAAGCAGAGAGAGAC 441  
 DB 361 AATAGAGATTAAGTGCAGAAAGACCTTGAATGAACAGATGCTGAAGCAGAGAGAGAC 420  
 QY 442 AAGATTAAAAAATATATCTCCAGAAAAAGAGAGCTCAGAGCACTATTTCTTTGT 501  
 DB 421 AAGATTAAAAAATATATCTCCAGAAAAAGAGAGCTCAGAGCACTATTTCTTTGT 480  
 QY 502 GATACCTGAACCTGCTAAGGCAATTAACAGAAAAAGAAAAATGAGAAAAAGACAA 561  
 DB 481 GATACCTGAACCTGCTAAGGCAATTAACAGAAAAAGAAAAATGAGAAAAAGACAA 540  
 QY 562 TCTATAGAGAGCTCCCACTTGAATTAAGTGAATGTAAGATGTTGATTCACCAAG 621  
 DB 541 TCTATAGAGAGCTCCCACTTGAATTAAGTGAATGTAAGATGTTGATTCACCAAG 600  
 QY 622 AATGAAAACGATGATGATTAATGATCTTACTAAGATGATGATGATGATGATGATGAT 681  
 DB 601 AATGAAAACGATGATGATTAATGATCTTACTAAGATGATGATGATGATGATGATGAT 660  
 QY 682 GATGATCCAGATGCTTCACTCACTAAGAGGAGCTCTTAAACGCTGAAGACATGTC 741

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Db      661 GATGATCCAGATGCTTTCATCATGACGAGGACTCCTTTAAACCGCTGAACATATGTC 720
QY      742 CATTAATTCGCTGCCAGATTTATATGAGAAATGACAGAGCCGTGTTGACAAGATTGTT 801
Db      721 CATTAATTCGCTGCCAGATTTATATGAGAAATGACAGAGCCGTGTTGACAAGATTGTT 780
QY      802 TCTAAACTACTTAATCTCGGCTTATCATCAGAAAGCAAGCATACATACCTGGAAATGAA 861
Db      781 TCTAAACTACTTAATCTCGGCTTATCATCAGAAAGCAAGCATACATACCTGGAAATGAA 840
QY      862 GTAGCAGAGGTTTTCACAAAATTAATCTCAAGAACCCACAAATATGAGAGATCC 921
Db      841 GTAGCAGAGGTTTTCACAAAATTAATCTCAAGAACCCACAAATATGAGAGATCC 900
QY      922 AATAAGCCACAGCTGGAGTGAATCAGCTGGAAAAATATCCAGAGAAAGTGCTCCA 981
Db      901 AATAAGCCACAGCTGGAGTGAATCAGCTGGAAAAATATCCAGAGAAAGTGCTCCA 960
QY      982 ATGCGAGCAATTCAGATGCTCTGCTAAGGAGAGAAACAGATGAACAGTATCTAACACA 1041
Db      961 ATGCGAGCAATTCAGATGCTCTGCTAAGGAGAGAAACAGATGAACAGTATCTAACACA 1020
QY      1042 TTAACCTTGACAAATGCGCTTGGAAGAGAACTAAACCTACAGTGAAGACACTTAA 1101
Db      1021 TTAACCTTGACAAATGCGCTTGGAAGAGAACTAAACCTACAGTGAAGACACTTAA 1080
QY      1102 GACTTCCAATATTTCCCAATTTCTATGCGCTACTGAAAGATATTTGATTCGAAAAAGAA 1161
Db      1081 GACTTCCAATATTTCCCAATTTCTATGCGCTACTGAAAGATATTTGATTCGAAAAAGAA 1140
QY      1162 GCAAAAGAGAAAGAAACACTGATTAATCATGAAACACATGATGACTTTGTGAAGATG 1221
Db      1141 GCAAAAGAGAAAGAAACACTGATTAATCATGAAACACATGATGACTTTGTGAAGATG 1200
QY      1222 ATGGTAATATGGAACAATATCTCCAGAAAGAGTGTTCCTACCTTGAAGAACTGGAT 1281
Db      1201 ATGGTAATATGGAACAATATCTCCAGAAAGAGTGTTCCTACCTTGAAGAACTGGAT 1260
QY      1282 GAAATGATGCTCTTCAGACCCAAACAGCTAGAAAAAATGCTACTGACATATATAGC 1341
Db      1261 GAAATGATGCTCTTCAGACCCAAACAGCTAGAAAAAATGCTACTGACATATATAGC 1320
QY      1342 AAGCTTTCCAGAGACCATGAGAAAGATCATGAAGAAACAGACAGTACCAAGAGAA 1401
Db      1321 AAGCTTTCCAGAGACCATGAGAAAGATCATGAAGAAACAGACAGTACCAAGAGAA 1380
QY      1402 GCACCTAAGATGGAAGAAATATGAAAGCTTGAAGATTCACAAAAGATGATATCC 1461
Db      1381 GCACCTAAGATGGAAGAAATATGAAAGCTTGAAGATTCACAAAAGATGATATCC 1440
QY      1462 AACCCAGAGAGAAAGACATGAACCCAAAGAAAAACAGAGCTATTTGGAAGCCATC 1521
Db      1441 AACCCAGAGAGAAAGACATGAACCCAAAGAAAAACAGAGCTATTTGGAAGCCATC 1500
QY      1522 AGAAAAATATATGATGTTGAAGAAACATGACAAAAGGAAATTAAGAAAGATATGAC 1581
Db      1501 AGAAAAATATATGATGTTGAAGAAACATGACAAAAGGAAATTAAGAAAGATATGAC 1560
QY      1582 CTTTCAAGATGAGAGACTTCATCAATTAACAAAGCTGATCTTATGGAAGAAAGCATC 1641
Db      1561 CTTTCAAGATGAGAGACTTCATCAATTAACAAAGCTGATCTTATGGAAGAAAGCATC 1620
QY      1642 CTTGACAGAGAAAGAGCCGAGCCATCAGCCGATTTATGACGCTGTAAAAATGGCAA 1701
Db      1621 CTTGACAGAGAAAGAGCCGAGCCATCAGCCGATTTATGACGCTGTAAAAATGGCAA 1680
QY      1702 AAGATCCAGAGATCTTCAACGTTTCAGAAAACATATATACCTTAAAAACATCTTAA 1761
Db      1681 AAGATCCAGAGATCTTCAACGTTTCAGAAAACATATATACCTTAAAAACATCTTAA 1740
QY      1762 TCTGTATTTAAATTTTTTGACCCAGAGGTTATTAAGAAAGTGTGAATTTACAGTATG 1821
Db      1741 TCTGTATTTAAATTTTTTGACCCAGAGGTTATTAAGAAAGTGTGAATTTACAGTATG 1800

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QY      1822 ACCTTTACAAAGTGTTAAACATAGCTTTCTCCCGTAAAAACATATCTGAAGTAAAGT 1881
Db      1801 ACCTTTACAAAGTGTTAAACATAGCTTTCTCCCGTAAAAACATATCTGAAGTAAAGT 1860
QY      1882 TGTATGTAAAGCTGACA 1897
Db      1861 TGTATGTAAAGCTGAAA 1876

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## RESULT 11

ACA63447  
ID ACA63447 standard; cDNA: 1893 BP.

ACA63447:

13-JUN-2003 (first entry)

DE cDNA encoding human PRO polypeptide #75.

KW Human: PRO polypeptide; secreted and transmembrane protein;

OS anti-PRO antibody; diagnostic assay; gene expression; gene; ss.

XX Homo sapiens.

XX US2003023042-A1.

XX 30-JAN-2003.

XX 01-MAY-2002; 2002US-0063502.

XX 06-DEC-2001; 2001US-0006867.

XX (GETH ) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX WPI: 2003-331484/31.

XX P-PSDB: AB072183.

PT Novel monoclonal antibody that binds to secreted and transmembrane  
PT polypeptide, useful for detecting and purifying the polypeptide and  
PT also for treating conditions responsive to the antibody

PS Disclosure: Fig 149; 408pp; English.

CC The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The  
CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides and polynucleotides are useful for preparing a  
CC medicament useful in the treatment of a condition responsive to  
CC anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic  
CC assays for PRO, by detecting its expression in specific cells,  
CC tissues or serum, and for affinity purification of PRO from  
CC recombinant cell culture or natural sources. ACA63373-ACA63456  
CC represent cDNA sequences encoding the human PRO polypeptides of  
CC the invention.

SO Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other;

Query Match 92.5%; Score 1866.4; DB 25; Length 1893;

Best local Similarity 99.7%; Pred. No. 0;

Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

QY      22 GTCCTCCGCTCACAGAACTTCAGACCCACAGGCGGACAGCGCTCCCTTACCTGGA 81
Db      1 GTCCTCCGCTCACAGAACTTCAGACCCACAGGCGGACAGCGCTCCCTTACCTGGA 60
QY      82 GACTTGACTCCGCGCGGCCCAACCCCTGTTATCCCTTGACCGTGAAGTGCAGAGATCC 141
Db      61 GACTTGACTCCGCGCGGCCCAACCCCTGTTATCCCTTGACCGTGAAGTGCAGAGATCC 120

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142 TGCAGCCGCGGAGTCCGCGGCTCTCCGCGCCACACCAACCTCTGGCTCTCTGT 201  
121 TGCAGCCGCGGAGTCCGCGGCTCTCCGCGCCACACCAACCTCTGGCTCTCTGT 180  
202 TTTTACT 261  
181 TTTTACT 240  
262 GTGACCCCAAGCCGAGCTGGAAGATGGGTTCTCTGCGGACCGGCACTTGTG 321  
241 GTGACCCCAAGCCGAGCTGGAAGATGGGTTCTCTGCGGACCGGCACTTGTG 300  
322 TTATGCTCCGATTTCAAGCTTTTCCCAACCTGGAGAACCAAGAAATCTTAAAT 381  
301 TTATGCTCCGATTTCAAGCTTTTCCCAACCTGGAGAACCAAGAAATCTTAAAT 360  
382 AATAGAGATTAATGTCAGAAAGACCTTGAATGAACGATTTGCTGAAGAGAAAG 441  
361 AATAGAGATTAATGTCAGAAAGACCTTGAATGAACGATTTGCTGAAGAGAAAG 420  
442 AAGATTAAGAAATATCTCTCAGAAAAACAGCGGTGAGCACTATTTCTTTGT 501  
421 AAGATTAAGAAATATCTCTCAGAAAAACAGCGGTGAGCACTATTTCTTTGT 480  
502 GATACCTGAACCTGCTAAGGCAATAACAGAAAAAGAAAAATTTGAAGAAAGAA 561  
481 GATACCTGAACCTGCTAAGGCAATAACAGAAAAAGAAAAATTTGAAGAAAGAA 540  
562 TCTTAAGAAAGCTCCGCACTTGAATTAATGATTTGAATGTAAGATTTGATTTCA 621  
541 TCTTAAGAAAGCTCCGCACTTGAATTAATGATTTGAATGTAAGATTTGATTTCA 600  
622 AATGAAATGATGATGATTAATGATGATGATGATGATGATGATGATGATGAT 681  
601 AATGAAATGATGATGATTAATGATGATGATGATGATGATGATGATGATGAT 660  
682 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 741  
661 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
742 CATAAATCGCTGCGAGATTTATGAAGAAATGACAGCGCTGTTGACAGATTT 801  
721 CATAAATCGCTGCGAGATTTATGAAGAAATGACAGCGCTGTTGACAGATTT 780  
802 TCTTAAGATGATTAATCTCGGCTTATCAGAGAAAGCAAGCATGAGAGATGA 861  
781 TCTTAAGATGATTAATCTCGGCTTATCAGAGAAAGCAAGCATGAGAGATGA 840  
862 GTACAGAGGTTTAAACAAATTAATCTCAAGAGAACCAACATTAATGAGAGATGCC 921  
841 GTACAGAGGTTTAAACAAATTAATCTCAAGAGAACCAACATTAATGAGAGATGCC 900  
922 AATAGCCCAAGCTGAGTGAAGATGAGCTGGAAGAAATATCAGAGAAAGTACTCA 981  
901 AATAGCCCAAGCTGAGTGAAGATGAGCTGGAAGAAATATCAGAGAAAGTACTCA 960  
982 ATGCGAGCATTTCAAGATGCTTGTCTAAGGAGAGAAACGATGAACGATTTCA 1041  
961 ATGCGAGCATTTCAAGATGCTTGTCTAAGGAGAGAAACGATGAACGATTTCA 1020  
1042 TTAACCTTGACAAATGGCTTGAAGAGGAACTTAACCTTACAGAGAAAGAACTTTAG 1101  
1021 TTAACCTTGACAAATGGCTTGAAGAGGAACTTAACCTTACAGAGAAAGAACTTTAG 1080  
1102 GACTTCCAAATTTTCCAAATTTCTATGCGCTACTGAAATATTTGATTTGAAAAAGAA 1161  
1081 GACTTCCAAATTTTCCAAATTTCTATGCGCTACTGAAATATTTGATTTGAAAAAGAA 1140  
1162 GCAAAAGAGAAAGAAACGATGATTAATGATTAAGAAACGATGATTTGTTGAGATG 1221  
1141 GCAAAAGAGAAAGAAACGATGATTAATGATTAAGAAACGATGATTTGTTGAGATG 1200  
1222 ATGCTGAATATGGAACATATCTCCAGAAAGAGTGTCTTCTTCTGAAACCTTGAT 1281

1201 ATGCTGAATATGGAACATATCTCTCAGAAAGAGTGTCTTCTTACTTGAACCTTGAT 1260  
1282 GAATGATTTGCTCTTCAAGACCAAAAAACAGCTAGAAAAAATGCTACTGACAAATAAGC 1341  
1261 GAATGATTTGCTCTTCAAGACCAAAAAACAGCTAGAAAAAATGCTACTGACAAATAAGC 1320  
1342 AAGCTTTTCCAGACCAATCAGAGAGAGTATGAAAGAAACAGACAGTACCAAGAGAA 1401  
1321 AAGCTTTTCCAGACCAATCAGAGAGAGTATGAAAGAAACAGACAGTACCAAGAGAA 1380  
1402 GCAGCTAAGATGAAAGAAAGATTTGAAAGCTTGAAGATTTCCACAAAGATGATTAATCC 1461  
1381 GCAGCTAAGATGAAAGAAAGATTTGAAAGCTTGAAGATTTCCACAAAGATGATTAATCC 1440  
1462 AACCCAGAGAGAAAGACAGATGAACCCCAAGAAAAACAGAAAGCTTATTTGAAAGCCATC 1521  
1441 AACCCAGAGAGAAAGACAGATGAACCCCAAGAAAAACAGAAAGCTTATTTGAAAGCCATC 1500  
1522 AGAAAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1581  
1501 AGAAAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
1582 CTTTCAAGATGAGAGACTTCAATCAATTAACAGCTGATGCTTATGAGAGAAAGGCAATC 1641  
1561 CTTTCAAGATGAGAGACTTCAATCAATTAACAGCTGATGCTTATGAGAGAAAGGCAATC 1620  
1642 CTTGCAAGAGAAAGAGCCGAGGCAATCAAGGCAATTTATGAGAGCTGTAATAAATGCGAA 1701  
1621 CTTGCAAGAGAAAGAGCCGAGGCAATCAAGGCAATTTATGAGAGCTGTAATAAATGCGAA 1680  
1702 AAGATCCAGAGCTCTTTAACTGTTTCAGAAAAACATTAATGATTTAAACATTTCTTAAT 1761  
1681 AAGATCCAGAGCTCTTTAACTGTTTCAGAAAAACATTAATGATTTAAACATTTCTTAAT 1740  
1762 TCTGATTAATAATTTTGAACCAAGGCTATTGAAGAGCTGAATTTACAGATTTA 1821  
1741 TCTGATTAATAATTTTGAACCAAGGCTATTGAAGAGCTGAATTTACAGATTTA 1800  
1822 ACCTTTTCAAGAGTGAATTAACATGATTTCTTCCGTAATAAATCTATCTGAAGTAAAGT 1881  
1801 ACCTTTTCAAGAGTGAATTAACATGATTTCTTCCGTAATAAATCTATCTGAAGTAAAGT 1860  
1882 TGTATGTAAGCTGAGA 1897  
1861 TGTATGTAAGCTGAAA 1876

RESULT 12  
ACA03647  
ID ACA03647 standard; cDNA; 1893 BP.  
XX  
AC ACA03647;  
XX  
DT 23-MAY-2003 (first entry)  
XX  
DE cDNA encoding human PRO polypeptide #45.  
KW Human; PRO polypeptide; secreted and transmembrane protein;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
KW differentiation; chondrocyte; tumour; genetic disorder;  
KW cytosolic; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2003036180-A1.  
XX  
PD 20-FEB-2003.  
XX  
XX 09-MAY-2002; 2002US-0143114.  
XX PF 31-MAR-1997; 97WO-US05230.  
XX PR 12-JUN-1998; 98WO-US12456.  
PR

14-JUL-1998; 98WO-US14552.  
 PR 28-AUG-1998; 98WO-US17888.  
 PR 10-SEP-1998; 98WO-US18824.  
 PR 14-SEP-1998; 98WO-US19093.  
 PR 14-SEP-1998; 98WO-US19094.  
 PR 14-SEP-1998; 98WO-US19177.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 17-SEP-1998; 98WO-US19437.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 29-OCT-1998; 98WO-US22992.  
 PR 20-NOV-1998; 98WO-US22992.  
 PR 01-DEC-1998; 98WO-US22855.  
 PR 05-JAN-1999; 98WO-US22108.  
 PR 08-MAR-1999; 98WO-US05190.  
 PR 10-MAR-1999; 98WO-US05190.  
 PR 20-APR-1999; 98WO-US08615.  
 PR 14-MAY-1999; 98WO-US10733.  
 PR 02-JUN-1999; 98WO-US12232.  
 PR 01-SEP-1999; 98WO-US20111.  
 PR 08-SEP-1999; 98WO-US20594.  
 PR 13-SEP-1999; 98WO-US20944.  
 PR 15-SEP-1999; 98WO-US21090.  
 PR 15-SEP-1999; 98WO-US21547.  
 PR 05-OCT-1999; 98WO-US23089.  
 PR 29-NOV-1999; 98WO-US28214.  
 PR 30-NOV-1999; 98WO-US28313.  
 PR 30-NOV-1999; 98WO-US28409.  
 PR 01-DEC-1999; 98WO-US28301.  
 PR 01-DEC-1999; 98WO-US28634.  
 PR 02-DEC-1999; 98WO-US28634.  
 PR 02-DEC-1999; 98WO-US28551.  
 PR 02-DEC-1999; 98WO-US28554.  
 PR 16-DEC-1999; 98WO-US28565.  
 PR 20-DEC-1999; 98WO-US30911.  
 PR 20-DEC-1999; 98WO-US30989.  
 PR 22-DEC-1999; 98WO-US30720.  
 PR 30-DEC-1999; 98WO-US31243.  
 PR 30-DEC-1999; 98WO-US31243.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 11-FEB-2000; 2000WO-US03736.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04342.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05746.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 21-MAR-2000; 2000WO-US07377.  
 PR 30-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 11-AUG-2000; 2000WO-US22031.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23522.  
 PR 08-NOV-2000; 2000WO-US33328.  
 PR 10-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.

PR 22-JUN-2001; 2001WO-US20116.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 20-DEC-2000; 2000WO-US074259.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 18-MAY-2001; 2001US-0860216.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 01-JUN-2001; 2001US-0872035.  
 PR 05-JUN-2001; 2001US-0874503.  
 PR 14-JUN-2001; 2001US-0882636.  
 PR 19-JUN-2001; 2001US-0882636.  
 PR 21-JUN-2001; 2001US-0887879.  
 PR 18-JUL-2001; 2001US-0908827.  
 PR 06-AUG-2001; 2001US-0924419.  
 PR 09-AUG-2001; 2001US-0927796.  
 PR 16-AUG-2001; 2001US-0931836.  
 PR 19-DEC-2001; 2001US-0028072.

## (GETH ) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 Gertlisen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 Smith V, Stewart TA, Tamas D, Watanabe CK, Wood WI, Zhang Z;  
 WPI: 2003-332040/31.  
 P-PSDB; AB066614.

New secreted and transmembrane PRO nucleic acids, useful for gene  
 therapy, in chromosome and gene mapping, as chromosome markers, in  
 tissue typing, and in chromosome identification  
 Claim 2; Fig 89; 660pp; English.

The present invention relates to the isolation of novel human PRO  
 polypeptides, and the polynucleotide sequences encoding them. The  
 PRO polypeptides are secreted and transmembrane proteins. The PRO  
 polypeptides are useful for detecting other PRO polypeptides, for  
 linking bioactive molecules to cells expressing PRO polypeptides,  
 for modulating biological activities of cells expressing PRO  
 polypeptides, and for identifying agonists or antagonists.  
 The PRO polypeptides are useful for stimulating the release of  
 tumour necrosis factor (TNF)-alpha from human blood, for stimulating  
 the proliferation or differentiation of chondrocytes, and detecting the  
 presence of tumours. The polynucleotide sequences encoding PRO  
 polypeptides are useful as hybridisation probes, in chromosome and  
 gene mapping, in the generation of antisense RNA and DNA, in the  
 preparation of PRO polypeptides, for generating transgenic animals or  
 knockout animals, for the genetic analysis of individuals with genetic  
 disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs  
 encoding the human PRO polypeptides of the invention.  
 Note: The sequence data for this patent was obtained in electronic  
 format directly from the USPTO web site at  
 seqdata.uspto.gov/psipsidentrity.html.

Sequence 1893 BP; 698 A; 389 G; 385 C; 421 T; 0 other.

Query Match 92.5%; Score 1866.4; DB 25; Length 1893;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 GTCCTCCGCTCAGACAGACTTCAGACCCAGAGGCGGAGCAGCGCTCCCTACCTGGA 81  
 Db 1 GTCCTCCGCTCAGACAGACTTCAGACCCAGAGGCGGAGCAGCGCTCCCTACCTGGA 60  
 QY 82 GACTTGACTCCCGCGCGCGCCCAACCCCTGCTTATCCCTTGACCGTGCAGAGATCC 141

61 GACTTGACTCCGGCGGCCCCAACCCCTGCTTATCCCTTGACCGTGAGTGTACAGATCC 120  
142 TGCAGCGCGCCAGTCCGGGCCCCCTCTCCGCCCCACACCCCTCTGCTCTTCTGT 201  
121 TGCAGCGCGCCAGTCCGGGCCCCCTCTCCGCCCCACACCCCTCTGCTCTTCTGT 180  
202 TTTTACTGCTCTCTTTTCTATCATTAACAAAGCTACAGTCCAGGAGGCCACGGCGGCT 261  
181 TTTTACTGCTCTCTTTTCTATCATTAACAAAGCTACAGTCCAGGAGGCCACGGCGGCT 240  
262 GTGACCCCAAGCCGAGCGTGAAGAATGGGGTTCCTCGGAGCCGGCAGCTTGTGATGCTG 321  
241 GTGACCCCAAGCCGAGCGTGAAGAATGGGGTTCCTCGGAGCCGGCAGCTTGTGATGCTG 300  
322 TTTAGTGTCCCGGATTTCAAGCTTTTCCCAACCTGGAGAGCCCAAGACAAATCTCTACAT 381  
301 TTTAGTGTCCCGGATTTCAAGCTTTTCCCAACCTGGAGAGCCCAAGACAAATCTCTACAT 360  
382 AATGAGAAATTAAGTGCAGAAAGACCTTGAATGACAGATTTGCTGAAGCAGAAAGAGC 441  
361 AATGAGAAATTAAGTGCAGAAAGACCTTGAATGACAGATTTGCTGAAGCAGAAAGAGC 420  
442 AAGATTAACAAAACATATCTCTCCAGAAAACAGCCAGGTCAGAGCAACTATCTTTTGT 501  
421 AAGATTAACAAAACATATCTCTCCAGAAAACAGCCAGGTCAGAGCAACTATCTTTTGT 480  
502 GATTAACCTTGAACTGCTGTAAGGCAATAACAGAAAAGAAAATTTGAGAAAAGACAA 561  
481 GATTAACCTTGAACTGCTGTAAGGCAATAACAGAAAAGAAAATTTGAGAAAAGACAA 540  
562 TCTTAAGAAAGCTCCCGCCTGATTAATGAATGTAATGTAAGATGTTGATTTCAACCAAG 621  
541 TCTTAAGAAAGCTCCCGCCTGATTAATGAATGTAATGTAAGATGTTGATTTCAACCAAG 600  
622 AATGCAAAACGTATGATGATTAATGATCTTAAGAGTGAATGGATCATTAATTTCAA 681  
601 AATGCAAAACGTATGATGATTAATGATCTTAAGAGTGAATGGATCATTAATTTCAA 660  
682 GATTAACCTTGAACTGCTGTAAGGCAATAACAGAAAAGAAAATTTGAGAAAAGACAA 741  
661 GATTAACCTTGAACTGCTGTAAGGCAATAACAGAAAAGAAAATTTGAGAAAAGACAA 720  
742 CATTAATAATCGTGCAGAGATTTAGAAAGAAATGACAGAGCGTGTGTAACAAAGATTT 801  
721 CATTAATAATCGTGCAGAGATTTAGAAAGAAATGACAGAGCGTGTGTAACAAAGATTT 780  
802 TCTTAACCTTAATCTCGGCTTATCAACAGAAAAGCCAGACATACACTGGAAGATGAA 861  
781 TCTTAACCTTAATCTCGGCTTATCAACAGAAAAGCCAGACATACACTGGAAGATGAA 840  
862 GTACACAGAGTTTTCACAAAATTAATCTCAAGAGAGCCACCAATTTAGAGAGATCCC 921  
841 GTACACAGAGTTTTCACAAAATTAATCTCAAGAGAGCCACCAATTTAGAGAGATCCC 900  
922 AATTAAGCCCAACAGCTGAGATCAGAAATCAGGCTGAAAATTAACAGAGAAATGACATCCA 981  
901 AATTAAGCCCAACAGCTGAGATCAGAAATCAGGCTGAAAATTAACAGAGAAATGACATCCA 960  
982 ATGGCAGCAATTTCAAGATGCTTCTGCTAAGGAGAGAAAAGATGAACAGATCTTAACACA 1041  
961 ATGGCAGCAATTTCAAGATGCTTCTGCTAAGGAGAGAAAAGATGAACAGATCTTAACACA 1020  
1042 TTAACCTTGACAAATGGCTTGAAGAGGAACTAAACCTTCAGTGAAGACAACTTTAGG 1101  
1021 TTAACCTTGACAAATGGCTTGAAGAGGAACTAAACCTTCAGTGAAGACAACTTTAGG 1080  
1102 GACTTCCAAATTTTCCCAAAATTTCTATGCGCTACTGAAAATTAATTTGATTTGAGAAAAGAA 1161  
1081 GACTTCCAAATTTTCCCAAAATTTCTATGCGCTACTGAAAATTAATTTGATTTGAGAAAAGAA 1140  
1162 GCAAAAAGAGAAAGAACTGATTAATCAATGAAGAACTGATTTGACTTTGTGAAGATG 1221  
1141 GCAAAAAGAGAAAGAACTGATTAATCAATGAAGAACTGATTTGACTTTGTGAAGATG 1200

1222 ATGGGAAATATGGAACAATATCTCCAGAAAGAGTGTTCCTTAACCTTGAACACTTGAT 1281  
1201 ATGGGAAATATGGAACAATATCTCCAGAAAGAGTGTTCCTTAACCTTGAACACTTGAT 1260  
1282 GAAATGATTTGCTCTTCAGACCCAAACAAAGCTAGAAAAAATGCTACTGACATATTAAGC 1341  
1261 GAAATGATTTGCTCTTCAGACCCAAACAAAGCTAGAAAAAATGCTACTGACATATTAAGC 1320  
1342 AAGCTTTTCCAGCACCATCAGAGAAAGATCATGAAGAAACAGACAGTACCAAGAGAA 1401  
1321 AAGCTTTTCCAGCACCATCAGAGAAAGATCATGAAGAAACAGACAGTACCAAGAGAA 1380  
1402 GCAGCTAAGATGGAAGAAAGATATGGAAGCTTGAAGATTCACAAAAAGATGATTAATCC 1461  
1381 GCAGCTAAGATGGAAGAAAGATATGGAAGCTTGAAGATTCACAAAAAGATGATTAATCC 1440  
1462 AACCAGAGAGAAAGACAGATGAACCCAAAGAAAACAGAAAGCTATTTGGAAGCCATC 1521  
1441 AACCAGAGAGAAAGACAGATGAACCCAAAGAAAACAGAAAGCTATTTGGAAGCCATC 1500  
1522 AGAAAAAATATGGAATGTTGAAGAAACATGACAAAAAGGAAATTAAGAAATTAATGAC 1581  
1501 AGAAAAAATATGGAATGTTGAAGAAACATGACAAAAAGGAAATTAAGAAATTAATGAC 1560  
1582 CTTTCAAGATGAGAGACTTGCATCAATTAACAGCTGTGCTTAATGAGAGAAAGGATC 1641  
1561 CTTTCAAGATGAGAGACTTGCATCAATTAACAGCTGTGCTTAATGAGAGAAAGGATC 1620  
1642 CTTGACAGAGAAAGCCGAGGCAATCAAGCCATTTATACACCTGTAAATAATGCA 1701  
1621 CTTGACAGAGAAAGCCGAGGCAATCAAGCCATTTATACACCTGTAAATAATGCA 1680  
1702 AAGATCCAGAGCTCTTCAACTGTTTCAGAAAACATTAATTAAGCTTAACACTTTAT 1761  
1681 AAGATCCAGAGCTCTTCAACTGTTTCAGAAAACATTAATTAAGCTTAACACTTTAT 1740  
1762 TCTGATTAATAATTTTGGACCAAGGCTTAATGAAGAGCTGAATTTACAGAGTAA 1821  
1741 TCTGATTAATAATTTTGGACCAAGGCTTAATGAAGAGCTGAATTTACAGAGTAA 1800  
1822 ACCTTTTCAGAGTGTAAACATAGCTTCTCCCTGAATAACATCTGAAGTAAAGT 1881  
1801 ACCTTTTCAGAGTGTAAACATAGCTTCTCCCTGAATAACATCTGAAGTAAAGT 1860  
1882 TGTATGTAAGCTGAGA 1897  
1861 TGTATGTAAGCTGAGA 1876  
RESULT 13  
ACA04068  
ID ACA04068 standard; cDNA; 1893 BP.  
XX  
AC ACA04068;  
XX  
DT 27-MAY-2003 (first entry)  
XX  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 89.  
XX  
KW Human; ss: gene; secreted protein; transmembrane protein; PRO;  
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
KW infertility; birth defects; premature aging; AIDS; biosensor;  
KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
KW bioeffector; tumour.  
XX  
OS Homo sapiens.  
XX  
PN US2003032155-A1.  
XX  
PD 13-FEB-2003.  
XX  
PF 03-MAY-2002; 2002US-0137865.

XX	31-MAR-1997;	5700-US05230
PR	12-JUN-1998;	9800-US12456
PR	14-AUG-1998;	9800-US14552
PR	28-JUL-1998;	9800-US17888
PR	10-SEP-1998;	9800-US18824
PR	14-SEP-1998;	9800-US19093
PR	14-SEP-1998;	9800-US19094
PR	16-SEP-1998;	9800-US19177
PR	17-SEP-1998;	9800-US19437
PR	07-OCT-1998;	9800-US21141
PR	29-OCT-1998;	9800-US22991
PR	29-OCT-1998;	9800-US22992
PR	20-NOV-1998;	9800-US24855
PR	01-DEC-1998;	9800-US25108
PR	05-JAN-1999;	9900-US00106
PR	08-MAR-1999;	9900-US05028
PR	10-MAR-1999;	9900-US05190
PR	20-APR-1999;	9900-US08615
PR	14-MAY-1999;	9900-US10733
PR	02-JUN-1999;	9900-US12352
PR	01-SEP-1999;	9900-US20111
PR	08-SEP-1999;	9900-US20594
PR	13-SEP-1999;	9900-US20944
PR	15-SEP-1999;	9900-US21090
PR	15-SEP-1999;	9900-US21547
PR	29-NOV-1999;	9900-US23089
PR	30-NOV-1999;	9900-US28214
PR	30-NOV-1999;	9900-US28313
PR	01-DEC-1999;	9900-US28409
PR	01-DEC-1999;	9900-US28301
PR	02-DEC-1999;	9900-US28551
PR	02-DEC-1999;	9900-US28564
PR	16-DEC-1999;	9900-US28565
PR	20-DEC-1999;	9900-US30095
PR	20-DEC-1999;	9900-US30911
PR	22-DEC-1999;	9900-US30999
PR	30-DEC-1999;	9900-US30720
PR	30-DEC-1999;	9900-US31243
PR	05-JAN-2000;	9900-US31274
PR	06-JAN-2000;	20000-US00219
PR	06-JAN-2000;	20000-US00277
PR	11-FEB-2000;	20000-US00366
PR	18-FEB-2000;	20000-US03555
PR	18-FEB-2000;	20000-US04341
PR	22-FEB-2000;	20000-US04342
PR	24-FEB-2000;	20000-US04914
PR	24-FEB-2000;	20000-US05004
PR	01-MAR-2000;	20000-US05601
PR	02-MAR-2000;	20000-US05746
PR	10-MAR-2000;	20000-US05841
PR	15-MAR-2000;	20000-US06319
PR	20-MAR-2000;	20000-US06884
PR	31-MAR-2000;	20000-US07377
PR	31-MAR-2000;	20000-US07532
PR	11-AUG-2000;	20000-US08439
PR	24-AUG-2000;	20000-US09328
PR	08-NOV-2000;	20000-US09592
PR	10-NOV-2000;	20000-US30875
PR	20-DEC-2000;	20000-US32678
PR	28-FEB-2001;	20000-US34956
PR	01-MAR-2001;	20000-US056520
		200100-US06656

25-MAY-2001; 2001MO-US17092.  
01-JUN-2001; 2001MO-US17800.  
20-JUN-2001; 2001MO-US19692.  
22-JUN-2001; 2001MO-US20116.  
29-JUN-2001; 2001MO-US21066.  
09-JUL-2001; 2001MO-US21735.  
20-DEC-2000; 2000US-0747255.  
28-FEB-2001; 2001US-0796498.  
09-MAR-2001; 2001US-0802706.  
14-MAR-2001; 2001US-0808689.  
22-MAR-2001; 2001US-0816744.  
05-APR-2001; 2001US-0828366.  
10-MAY-2001; 2001US-0854208.  
10-MAY-2001; 2001US-0854280.  
18-MAY-2001; 2001US-0860216.  
25-MAY-2001; 2001US-0866028.  
25-MAY-2001; 2001US-0866034.  
01-JUN-2001; 2001US-0872035.  
05-JUN-2001; 2001US-0874503.  
14-JUN-2001; 2001US-0882636.  
19-JUN-2001; 2001US-0886342.  
21-JUN-2001; 2001US-0887879.  
18-JUL-2001; 2001US-0908827.  
06-AUG-2001; 2001US-0924419.  
09-AUG-2001; 2001US-0927796.  
16-AUG-2001; 2001US-0931836.  
19-DEC-2001; 2001US-0028072.

(GETH ) GENENTECH INC.

Baker RP, Beresini M, DeForge L, Desnoyers L, Flivaroff E, Gao W, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S, Smith V, Stewart RA, Tumas D, Watanabe CK, Wood WT, Zhang Z; WPI: 2003-331925/31.  
P-PSDB: AB066890.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer -

Claim 2; Fig 89; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited under American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host cells for producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO extracellular domains and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TNF-alpha (tumor necrosis factor alpha) from human blood, and the proliferation of differentiation of chondrocyte cells, the proliferation of, or gene expression in pericyte cells, the release or proteoglycans from cartilage, proliferation of inner ear utricular supporting cells, the proliferation of T-lymphocyte cells, the release of a cytokine from peripheral blood mononuclear cells (PBMC), or the proliferation of endothelial cells), a method for modulating the uptake of glucose or free fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the binding of A-peptide to factor VIIA, or the differentiation of adipocyte cells, a method for detecting the presence of a tumor in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences cited above. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioeffectors. Both are useful in tissue typing





XX Human; PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.  
OS Homo sapiens.  
XX  
XX US2003017563-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 07-MAY-2002; 2002US-0140808.  
XX  
PR 31-MAR-1997; 97WO-US05230.  
PR 12-JUN-1998; 98WO-US12456.  
PR 14-JUL-1998; 98WO-US14552.  
PR 28-AUG-1998; 98WO-US17888.  
PR 10-SEP-1998; 98WO-US18824.  
PR 14-SEP-1998; 98WO-US19093.  
PR 14-SEP-1998; 98WO-US19094.  
PR 16-SEP-1998; 98WO-US19177.  
PR 17-SEP-1998; 98WO-US19177.  
PR 07-OCT-1998; 98WO-US19437.  
PR 29-OCT-1998; 98WO-US21141.  
PR 29-OCT-1998; 98WO-US22991.  
PR 20-NOV-1998; 98WO-US22992.  
PR 01-DEC-1998; 98WO-US24855.  
PR 05-JAN-1999; 98WO-US25108.  
PR 08-MAR-1999; 98WO-US25106.  
PR 10-MAR-1999; 98WO-US25028.  
PR 20-APR-1999; 98WO-US25190.  
PR 14-MAY-1999; 98WO-US2508615.  
PR 02-JUN-1999; 98WO-US2510733.  
PR 01-SEP-1999; 98WO-US2512252.  
PR 08-SEP-1999; 98WO-US250111.  
PR 13-SEP-1999; 98WO-US250594.  
PR 15-SEP-1999; 98WO-US21090.  
PR 05-OCT-1999; 98WO-US21547.  
PR 29-NOV-1999; 98WO-US23089.  
PR 30-NOV-1999; 98WO-US28214.  
PR 01-DEC-1999; 98WO-US28313.  
PR 01-DEC-1999; 98WO-US28409.  
PR 01-DEC-1999; 98WO-US28301.  
PR 02-DEC-1999; 98WO-US28634.  
PR 02-DEC-1999; 98WO-US28551.  
PR 02-DEC-1999; 98WO-US28564.  
PR 16-DEC-1999; 98WO-US28565.  
PR 20-DEC-1999; 98WO-US30095.  
PR 20-DEC-1999; 98WO-US30911.  
PR 22-DEC-1999; 98WO-US30999.  
PR 30-DEC-1999; 98WO-US31243.  
PR 30-DEC-1999; 98WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 11-FEB-2000; 2000WO-US00376.  
PR 18-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 22-FEB-2000; 2000WO-US04342.  
PR 24-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 01-MAR-2000; 2000WO-US05004.  
PR 02-MAR-2000; 2000WO-US05746.  
PR 02-MAR-2000; 2000WO-US05841.

PR 10-MAR-2000; 2000WO-US06319.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 11-AUG-2000; 2000WO-US22031.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 22-JUN-2001; 2001WO-US20116.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 20-DEC-2000; 2000US-0747259.  
PR 28-FEB-2001; 2001US-0796498.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 18-MAY-2001; 2001US-0860216.  
PR 23-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 01-JUN-2001; 2001US-0872035.  
PR 05-JUN-2001; 2001US-0874503.  
PR 14-JUN-2001; 2001US-0882636.  
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PR 09-AUG-2001; 2001US-0927796.  
PR 16-AUG-2001; 2001US-0931836.  
PR 19-DEC-2001; 2001US-0028072.  
XX  
XX (GENTH ) GENENTECH INC.  
XX  
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
XX Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX WPI; 2003-148238/14.  
XX P-PSDB; AB059695.  
XX  
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
XX are therapeutically useful for enhancing immune response and in cancer  
XX treatments  
XX  
XX Claim 2; Fig 89; 659pp; English.  
XX  
XX The invention describes an isolated human PRO polypeptide. The PRO  
XX polypeptides are useful in detecting PRO polypeptides in a sample, in  
XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
XX in modulating at least one biological activity of a cell expressing a PRO  
XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
XX stimulate adrenal cortical insufficiency disorders. PRO154 and PRO136,  
XX PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
XX useful for treating conditions or disorders where angiogenesis would be

CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC useful for treating cancerous tumours. PRO812 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO26,  
CC PRO1066, PRO1384, PRO1366 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
CC immune response. PRO826, PRO1066 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813  
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and  
CC are thus useful for treating sports injuries, and arthritis. This  
CC sequence encodes a novel human PRO protein.

xx Sequence 1893 BP: 698 A: 389 C: 385 G: 421 T: 0 other:

Query Match 92.5%; Score 1866.4; DB 25; Length 1893;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1870: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 GTCTCCGGGTACAGAACTTCAGCACCACAGGCGGACAGCGCTCCCTCTACCTGGA 81  
DB 1 GTCTCCGGGTACAGAACTTCAGCACCACAGGCGGACAGCGCTCCCTCTACCTGGA 60  
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DB 61 GACTTGACTCCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120  
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DB 121 TGACAGCCCGCAGTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
QY 202 TTTTACT 261  
DB 181 TTTTACT 240  
QY 262 GTGACCCCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 321  
DB 241 GTGACCCCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
QY 322 TTAGTGTCTCCGATTCAGCTTTTCCCAACCTGAGAGGCGGCGGCGGCGGCGGCGGCGG 381  
DB 301 TTAGTGTCTCCGATTCAGCTTTTCCCAACCTGAGAGGCGGCGGCGGCGGCGGCGGCGG 360  
QY 382 AATAGAGATTAAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAGAGAC 441  
DB 361 AATAGAGATTAAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAGAGAC 420  
QY 442 AAGATTAAAGAAACATATCTCCAGAAACAAAGCGGCGGCGGCGGCGGCGGCGGCGG 501  
DB 421 AAGATTAAAGAAACATATCTCCAGAAACAAAGCGGCGGCGGCGGCGGCGGCGGCGG 480  
QY 502 GATACTTGAACCTGCTTAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 561  
DB 481 GATACTTGAACCTGCTTAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540  
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DB 541 TCTATAGAGAGCTCCCGCAGTTGATTAAGTTGAATGGAAGATGTTGATTAACCAAG 600  
QY 622 AATGGAAGAGATGATGATTAAGTACTCTAAGATGATGATGATGATGATGATGATGAT 681  
DB 601 AATGGAAGAGATGATGATTAAGTACTCTAAGATGATGATGATGATGATGATGATGATGAT 660  
QY 682 GATGATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 741  
DB 661 GATGATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720

QY 742 CATAAATCGCTGCGGAGATTTATGAGAAATGACAGAGCGGTGTTGACAGATGTTGT 801  
DB 721 CATAAATCGCTGCGGAGATTTATGAGAAATGACAGAGCGGTGTTGACAGATGTTGT 780  
QY 802 TCTAACTACTTAATCTGCGGCTTTCACAGAAAGCCAGACATACATGAGAGATGAA 861  
DB 781 TCTAACTACTTAATCTGCGGCTTTCACAGAAAGCCAGACATACATGAGAGATGAA 840  
QY 862 GTAGCAGAGGTTTACAAAATTAATTCGAAAGAGCCAGACATTAATGAGAGATCCC 921  
DB 841 GTAGCAGAGGTTTACAAAATTAATTCGAAAGAGCCAGACATTAATGAGAGATCCC 900  
QY 922 AATAAGCCACAGAGTGCAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 981  
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QY 1642 CTTGACAG 1701  
DB 1621 CTTGACAG 1680  
QY 1702 AAGATCCAGAGAGCTTTTCAAGCTGTTGAGAAAGCAATATATAGCTTAAACAGCTCTAT 1761  
DB 1681 AAGATCCAGAGAGCTTTTCAAGCTGTTGAGAAAGCAATATATAGCTTAAACAGCTCTAT 1740  
QY 1762 TCTGATTAATAATTTTGAAGAGAGGATTAAGAAAGTGTGATTAACAGTATGTA 1821  
DB 1741 TCTGATTAATAATTTTGAAGAGAGGATTAAGAAAGTGTGATTAACAGTATGTA 1800

OY 1822 ACCTTTACAGTGTAAACATAGCTTCTCCGTAATAAAGTGAAGTAAGT 1881  
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DB 1801 ACCTTTACAGTGTAAACATAGCTTCTCCGTAATAAAGTGAAGTAAGT 1860  
OY 1882 TGTATGTAGCTGAGA 1897  
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DB 1861 TGTATGTAGCTGAGA 1876

## RESULT 15

AAK94872  
ID AAK94872 standard; cDNA: 1871 BP.

XX AAK94872;

DT 06-NOV-2001 (first entry)

DE Human full-length cDNA, SEQ ID NO: 4060.

KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

OS Homo sapiens.

PN EP130094-A2.

PD 05-SEP-2001.

PF 07-JUL-2000; 2000EP-0114089.

PR 08-JUL-1999; 99JP-0194486.

PR 11-JAN-2000; 2000JP-0118774.

PR 02-MAY-2000; 2000JP-0183765.

XX (HELI-) HELIX RES INST.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Makematsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

DR WPI: 2001-524255/58.

DR P-PSDB: AAM93910.

XX 830 Primers useful for synthesizing full length cDNA clones and their

PT use in genetic manipulation -

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OY 144 CAGCCGCCAGTCCCGGCCCTCTCCGCCACACACCCTCTGCTCTCTGTT 203  
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OY 204 TTACTCCCTCTTTCATTCATTAACAAAAGCTACAGCTCCAGAGCCCGGCTGT 263  
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OY 444 GATTAAAAAAACATATCTCCAGAAAACAGCCAGTCCAGAGCACTATCTTTGTGTA 503  
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Db 1561 TTCAAGATGAGAGACTTCATCAATTAACAAGCTGATGCTATGTGAGAAAAAGCATCCT 1620
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

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(without alignments)  
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Title: US-09-554-945B-2

Perfect score: 2402

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Searched: 510680 seqs, 136781880 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	2384	99.3	468	12	US-10-035-977-67
3	2384	99.3	468	12	US-10-063-735-150
4	2384	99.3	468	12	US-10-137-870-90
5	2384	99.3	468	12	US-10-140-018-90
6	2384	99.3	468	12	US-10-140-021-90
7	2384	99.3	468	12	US-10-140-274-90
8	2384	99.3	468	12	US-10-140-471-90
9	2384	99.3	468	12	US-10-140-807-90
10	2384	99.3	468	12	US-10-140-922-90
11	2384	99.3	468	12	US-10-140-924-90
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17	2384	99.3	468	12	US-10-142-432-90	Sequence 90, Appl
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41	2384	99.3	468	12	US-10-147-529-90	Sequence 90, Appl
42	2384	99.3	468	12	US-10-152-357-90	Sequence 90, Appl
43	2384	99.3	468	12	US-10-153-586-90	Sequence 90, Appl
44	2384	99.3	468	12	US-10-158-783-90	Sequence 90, Appl
45	2384	99.3	468	12	US-10-158-786-90	Sequence 90, Appl

#### ALIGNMENTS

```

US-09-931-836-67
; Sequence 67, Application US/09931836
; Publication No. US20030027249A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gueney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: ACIDED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C1
; CURRENT APPLICATION NUMBER: US/09/931, 836
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22

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;; PRIOR APPLICATION NUMBER: 60/125774  
;; PRIOR FILING DATE: 1999-03-23  
;; PRIOR APPLICATION NUMBER: 60/125778  
;; PRIOR FILING DATE: 1999-03-23  
;; PRIOR APPLICATION NUMBER: 60/125886  
;; PRIOR FILING DATE: 1999-03-24  
;; PRIOR APPLICATION NUMBER: 60/127035  
;; PRIOR FILING DATE: 1999-03-31  
;; PRIOR APPLICATION NUMBER: 60/127706  
;; PRIOR FILING DATE: 1999-04-05  
;; PRIOR APPLICATION NUMBER: 60/129122  
;; PRIOR FILING DATE: 1999-04-13  
;; PRIOR APPLICATION NUMBER: 60/130359  
;; PRIOR FILING DATE: 1999-04-21  
;; PRIOR APPLICATION NUMBER: 60/131270  
;; PRIOR FILING DATE: 1999-04-27  
;; PRIOR APPLICATION NUMBER: 60/131272  
;; PRIOR FILING DATE: 1999-04-27  
;; PRIOR APPLICATION NUMBER: 60/131291  
;; PRIOR FILING DATE: 1999-04-27  
;; PRIOR APPLICATION NUMBER: 60/132371  
;; PRIOR FILING DATE: 1999-05-04  
;; PRIOR APPLICATION NUMBER: 60/132379  
;; PRIOR FILING DATE: 1999-05-04  
;; PRIOR APPLICATION NUMBER: 60/132383  
;; PRIOR FILING DATE: 1999-05-04  
;; PRIOR APPLICATION NUMBER: 60/135750  
;; PRIOR FILING DATE: 1999-05-25  
;; PRIOR APPLICATION NUMBER: 60/138166  
;; PRIOR FILING DATE: 1999-06-08  
;; PRIOR APPLICATION NUMBER: 60/144791  
;; PRIOR FILING DATE: 1999-07-20  
;; PRIOR APPLICATION NUMBER: 60/146970  
;; PRIOR FILING DATE: 1999-08-03  
;; PRIOR APPLICATION NUMBER: 60/162506  
;; PRIOR FILING DATE: 1999-10-29  
;; PRIOR APPLICATION NUMBER: 09/311832  
;; PRIOR FILING DATE: 1999-05-14  
;; PRIOR APPLICATION NUMBER: 09/380142  
;; PRIOR FILING DATE: 1999-08-25  
;; PRIOR APPLICATION NUMBER: 09/644848  
;; PRIOR FILING DATE: 2000-08-22  
;; PRIOR APPLICATION NUMBER: 09/747259  
;; PRIOR FILING DATE: 2000-12-20  
;; PRIOR APPLICATION NUMBER: 09/816744  
;; PRIOR FILING DATE: 2001-03-22  
;; PRIOR APPLICATION NUMBER: 09/854208  
;; PRIOR FILING DATE: 2001-05-10  
;; PRIOR APPLICATION NUMBER: 09/854280  
;; PRIOR FILING DATE: 2001-05-10  
;; PRIOR APPLICATION NUMBER: 09/874503  
;; PRIOR FILING DATE: 2001-06-05  
;; PRIOR APPLICATION NUMBER: 09/869599  
;; PRIOR FILING DATE: 2001-06-29  
;; PRIOR APPLICATION NUMBER: 09/908,827  
;; PRIOR FILING DATE: 2001-07-18  
;; PRIOR APPLICATION NUMBER: PCT/US99/10733  
;; PRIOR FILING DATE: 1999-05-14  
;; PRIOR APPLICATION NUMBER: PCT/US99/28551  
;; PRIOR FILING DATE: 1999-12-02  
;; PRIOR APPLICATION NUMBER: PCT/US99/30720  
;; PRIOR FILING DATE: 1999-12-22  
;; PRIOR APPLICATION NUMBER: PCT/US00/05601  
;; PRIOR FILING DATE: 2000-03-01  
;; PRIOR APPLICATION NUMBER: PCT/US00/05841  
;; PRIOR FILING DATE: 2000-03-02  
;; PRIOR APPLICATION NUMBER: PCT/US00/14042  
;; PRIOR FILING DATE: 2000-05-22  
;; PRIOR APPLICATION NUMBER: PCT/US00/15264  
;; PRIOR FILING DATE: 2000-06-02  
;; PRIOR APPLICATION NUMBER: PCT/US00/23522  
;; PRIOR FILING DATE: 2000-08-23  
;; PRIOR APPLICATION NUMBER: PCT/US00/23328

;; PRIOR FILING DATE: 2000-08-24  
;; PRIOR APPLICATION NUMBER: PCT/US00/32678  
;; PRIOR FILING DATE: 2000-12-01  
;; PRIOR APPLICATION NUMBER: PCT/US00/34956  
;; PRIOR FILING DATE: 2000-12-20  
;; PRIOR APPLICATION NUMBER: PCT/US01/06520  
;; PRIOR FILING DATE: 2001-06-28  
;; PRIOR APPLICATION NUMBER: PCT/US01/17800  
;; PRIOR FILING DATE: 2001-06-01  
;; PRIOR APPLICATION NUMBER: PCT/US01/19692  
;; PRIOR FILING DATE: 2001-06-20  
;; PRIOR APPLICATION NUMBER: PCT/US01/21066  
;; PRIOR FILING DATE: 2001-06-29  
;; PRIOR APPLICATION NUMBER: PCT/US01/21735  
;; PRIOR FILING DATE: 2001-07-09  
;; NUMBER OF SEQ ID NOS: 80  
;; SEQ ID NO 67  
;; LENGTH: 468  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-09-931-836-67

Query Match 99.3%; Score 2384; DB 11; Length 468;  
Best Local Similarity 99.1%; Pred. No. 1,2e-152;  
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFCTGTLVILVLPLOAFPPKPGSODKSLHNRRLSAERPLNEQIAEAEDEKIKKTYPP 60  
DB 1 MGFCTGTLVILVLPLOAFPPKPGSODKSLHNRRLSAERPLNEQIAEAEDEKIKKTYPP 60  
QY 61 ENKPGQSNYSFVNDNLNRAITTEKERTEKEROSIRSSPLDNKLNVEDVSTKRRKLIIDY 120  
DB 61 ENKPGQSNYSFVNDNLNRAITTEKERTEKEROSIRSSPLDNKLNVEDVSTKRRKLIIDY 120  
QY 121 DSTKSGLDHKEFQDDPDGLHOLDGTPLEADIVKIKARIYEENDRAVFDKIVSKLNLGL 180  
DB 121 DSTKSGLDHKEFQDDPDGLHOLDGTPLEADIVKIKARIYEENDRAVFDKIVSKLNLGL 180  
QY 181 ITTSQAHTLDEVAEYVLOKLSKEANNYEEDPKPISWTENOAGKIPKVTYPAAIQDGL 240  
DB 181 ITTSQAHTLDEVAEYVLOKLSKEANNYEEDPKPISWTENOAGKIPKVTYPAAIQDGL 240  
QY 241 AKGENDETYSNTLTNLNGLEBRRTKTYSEDNFRDFOYEPNRYALNLSIDSEKKEKETLI 300  
DB 241 AKGENDETYSNTLTNLNGLEBRRTKTYSEDNFRDFOYEPNRYALNLSIDSEKKEKETLI 300  
QY 301 TIMKTLLIDFVKMVKYGTISPREGVSYLENLDEMIALQTKNLEKNATDNISKLPAPSE 360  
DB 301 TIMKTLLIDFVKMVKYGTISPREGVSYLENLDEMIALQTKNLEKNATDNISKLPAPSE 360  
QY 361 KSHETDSTRKEPAKKEKESYSLKDTKDNDSNPGKCTDEPKGTIYALIRKNIEMWL 420  
DB 361 KSHETDSTRKEPAKKEKESYSLKDTKDNDSNPGKCTDEPKGTIYALIRKNIEMWL 420  
QY 421 KHDKKNKEDYDLSKMRDEINKQADAYVEKGLIDKEEAPAKRITYSSL 468  
DB 421 KHDKKNKEDYDLSKMRDEINKQADAYVEKGLIDKEEAPAKRITYSSL 468

RESULT 2  
US-10-035-977-67  
; Sequence 67, Application US/10035977  
; Publication No. US20030134327A1  
; GENERAL INFORMATION:  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.



```

? PRIOR FILING DATE: 2001-05-10
? PRIOR APPLICATION NUMBER: 09/874503
? PRIOR FILING DATE: 2001-06-05
? PRIOR APPLICATION NUMBER: 09/869599
? PRIOR FILING DATE: 2001-06-29
? PRIOR APPLICATION NUMBER: 09/908, 827
? PRIOR FILING DATE: 2001-07-18
? PRIOR APPLICATION NUMBER: PCT/US99/10733
? PRIOR FILING DATE: 1999-05-14
? PRIOR APPLICATION NUMBER: PCT/US99/28551
? PRIOR FILING DATE: 1999-12-02
? PRIOR APPLICATION NUMBER: PCT/US99/30720
? PRIOR FILING DATE: 1999-12-22
? PRIOR APPLICATION NUMBER: PCT/US00/05601
? PRIOR FILING DATE: 2000-03-01
? PRIOR APPLICATION NUMBER: PCT/US00/05841
? PRIOR FILING DATE: 2000-03-02
? PRIOR APPLICATION NUMBER: PCT/US00/14042
? PRIOR FILING DATE: 2000-05-22
? PRIOR APPLICATION NUMBER: PCT/US00/15264
? PRIOR FILING DATE: 2000-06-02
? PRIOR APPLICATION NUMBER: PCT/US00/23522
? PRIOR FILING DATE: 2000-08-23
? PRIOR APPLICATION NUMBER: PCT/US00/23328
? PRIOR FILING DATE: 2000-08-24
? PRIOR APPLICATION NUMBER: PCT/US00/32678
? PRIOR FILING DATE: 2000-12-01
? PRIOR APPLICATION NUMBER: PCT/US00/34956
? PRIOR FILING DATE: 2000-12-20
? PRIOR APPLICATION NUMBER: PCT/US01/06520
? PRIOR FILING DATE: 2001-02-28
? PRIOR APPLICATION NUMBER: PCT/US01/17800
? PRIOR FILING DATE: 2001-06-01
? PRIOR APPLICATION NUMBER: PCT/US01/19692
? PRIOR FILING DATE: 2001-06-20
? PRIOR APPLICATION NUMBER: PCT/US01/21066
? PRIOR FILING DATE: 2001-06-29
? PRIOR APPLICATION NUMBER: PCT/US01/21735
? PRIOR FILING DATE: 2001-07-09
? NUMBER OF SEQ ID NOS: 80
? SEQ ID NO 67
? LENGTH: 468
? TYPE: PRF
? ORGANISM: Homo Sapien
? US-10-035-977-67

Query Match          99.3%   Score 2384; DB 12; Length 468:
Best Local Similarity    99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative      2; Mismatches     2; Indels       0; Gaps        0;

QY      1 MGFLGTGMIIVLYLPFIQAFFPKPGSQSKSLHNRELISAERPLNEQIAEAEDKIKTYPP 60
DB      1 MGFLGTGWILVLYLPIAFAFPKPQSOKSLHNRRLSARPLNEDIABAEDEKIITYPP 60

QY      61 ENRFGQQSNYSFVDNLINLRATIEREKIEKEROSIRSSPDLNKLVNEYDSTRKKLLIDY 120
DB      61 ENRFGQQSNYSFYNDLNLIKAITTEKEIKEKRQSISSPSLDKNLANEYDVSTRNKLIDDY 120

QY      121 DSTSYSGLDHKRODDPDGGJHOJDGPFLTAEDTVHYKLAARIYEENDAVAEDKYISKLTNLGL 180
DB      121 DSTSASGDHKKRDDDPDGJHOJDGPLTAAEDTVHYKLAARIYEENDAVADKYISKTNLGL 180

QY      181 ITTESOAHRTLEBEVAEVLODKLISTSEANNANEEDPNRPPTSWTENOGAKIPEKVTPMAIQDGL 240
DB      181 ITTESOAHTLEBEVAEVLODKLISTSEANNNAYEEDPNRKPTSMTBNOAGKITPEKVTPMIIAQDGL 240

QY      241 AKGENDETVSNTTLFTINGLERRTKTYSEDNFDFQYPFNRYALALKSIDSEKAEEKETLI 300
DB      241 AKGENDETVSNTTLFTINGLERRTKTYSDDNFEELDYFPNFYAALLKSIDSKEAKEKETLI 300

QY      301 TTKMTITLIDFYVMARKYGTSISEEGSVYLENIDEMIALOTKKKLEKANATDINSKLFPAESE 360
DB      301 TTKMTITLIDFYVMARKYGTSISEEGSVYLENIDEMIALOTKKKLEKANATDINSKLFPAESE 360

```

```
OY 361 KSHETDSTKEAAKKEEYGLKSTKDNNSPGKTEDEPKTEAYLEAIRKNTEWLK 420
|||
Db 361 KSHETDSTKEAAKKEEYGLKSTKDNNSPGKTEDEPKTEAYLEAIRKNTEWLK 420
OY 421 KHKGNKEDYDLSKMRDPIFKQADAYVEKGIIDKEEAIRKRIYSSL 468
|||
Db 421 KHKGNKEDYDLSKMRDPIFKQADAYVEKGIIDKEEAIRKRIYSSL 468
```

## RESULT 3

```
US-10-063-735-150
; Sequence 150, Application US/10063735
; Publication No. US20030138882A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William T.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,735
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 150
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-735-150
```

```
Query Match 99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1,2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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OY 1 MGFLGTGWTILVLPFIOAFPKPGSQDSSLNRELASRPINQIAEAEDKIKKTYPP 60
|||
Db 1 MGFLGTGWTILVLPFIOAFPKPGSQDSSLNRELASRPINQIAEAEDKIKKTYPP 60
OY 61 ENKPGQSNYSFVDNLNLKAITTEKEKIEKERSIRSSPLDNKLNVEDVSTKNRKLIDY 120
|||
Db 61 ENKPGQSNYSFVDNLNLKAITTEKEKIEKERSIRSSPLDNKLNVEDVSTKNRKLIDY 120
OY 121 DSTKSGLDHKFODDPDGLHQLDGTPLTAEDIYHKIARIYEENDRAVFDKIVSKLLNLGL 180
|||
Db 121 DSTKSGLDHKFODDPDGLHQLDGTPLTAEDIYHKIARIYEENDRAVFDKIVSKLLNLGL 180
OY 181 ITESQAHTLEDEVAEYLOKLISKEANNYEEDPNKPTSWTENQAKIPEKVTMAAIODGL 240
|||
Db 181 ITESQAHTLEDEVAEYLOKLISKEANNYEEDPNKPTSWTENQAKIPEKVTMAAIODGL 240
OY 241 AKGENDETVSNLTLTNGLERTKTYSEDNFEELQYFPNFYALLKSIDSEKAEKETLI 300
|||
Db 241 AKGENDETVSNLTLTNGLERTKTYSEDNFEELQYFPNFYALLKSIDSEKAEKETLI 300
OY 301 TIMKTLIDFVKMVKYGTISPPEGVSYLENLDEMIALQTKNKLKKNATONISKLFPAPSE 360
|||
Db 301 TIMKTLIDFVKMVKYGTISPPEGVSYLENLDEMIALQTKNKLKKNATONISKLFPAPSE 360
OY 361 KSHETDSTKEAAKKEEYGLKSTKDNNSPGKTEDEPKTEAYLEAIRKNTEWLK 420
|||
Db 361 KSHETDSTKEAAKKEEYGLKSTKDNNSPGKTEDEPKTEAYLEAIRKNTEWLK 420
OY 421 KHKGNKEDYDLSKMRDPIFKQADAYVEKGIIDKEEAIRKRIYSSL 468
|||
Db 421 KHKGNKEDYDLSKMRDPIFKQADAYVEKGIIDKEEAIRKRIYSSL 468
```

```
RESULT 4
US-10-137-870-90
; Sequence 90, Application US/10137870
; Publication No. US20030138883A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Laureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C155
; CURRENT APPLICATION NUMBER: US/10/137,870
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 90
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-870-90
```

```
Query Match 99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1,2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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OY 1 MGFLGTGWTILVLPFIOAFPKPGSQDSSLNRELASRPINQIAEAEDKIKKTYPP 60
|||
Db 1 MGFLGTGWTILVLPFIOAFPKPGSQDSSLNRELASRPINQIAEAEDKIKKTYPP 60
OY 61 ENKPGQSNYSFVDNLNLKAITTEKEKIEKERSIRSSPLDNKLNVEDVSTKNRKLIDY 120
|||
Db 61 ENKPGQSNYSFVDNLNLKAITTEKEKIEKERSIRSSPLDNKLNVEDVSTKNRKLIDY 120
OY 121 DSTKSGLDHKFODDPDGLHQLDGTPLTAEDIYHKIARIYEENDRAVFDKIVSKLLNLGL 180
|||
Db 121 DSTKSGLDHKFODDPDGLHQLDGTPLTAEDIYHKIARIYEENDRAVFDKIVSKLLNLGL 180
OY 181 ITESQAHTLEDEVAEYLOKLISKEANNYEEDPNKPTSWTENQAKIPEKVTMAAIODGL 240
|||
Db 181 ITESQAHTLEDEVAEYLOKLISKEANNYEEDPNKPTSWTENQAKIPEKVTMAAIODGL 240
OY 241 AKGENDETVSNLTLTNGLERTKTYSEDNFEELQYFPNFYALLKSIDSEKAEKETLI 300
|||
Db 241 AKGENDETVSNLTLTNGLERTKTYSEDNFEELQYFPNFYALLKSIDSEKAEKETLI 300
OY 301 TIMKTLIDFVKMVKYGTISPPEGVSYLENLDEMIALQTKNKLKKNATONISKLFPAPSE 360
|||
Db 301 TIMKTLIDFVKMVKYGTISPPEGVSYLENLDEMIALQTKNKLKKNATONISKLFPAPSE 360
OY 361 KSHETDSTKEAAKKEEYGLKSTKDNNSPGKTEDEPKTEAYLEAIRKNTEWLK 420
|||
Db 361 KSHETDSTKEAAKKEEYGLKSTKDNNSPGKTEDEPKTEAYLEAIRKNTEWLK 420
OY 421 KHKGNKEDYDLSKMRDPIFKQADAYVEKGIIDKEEAIRKRIYSSL 468
|||
Db 421 KHKGNKEDYDLSKMRDPIFKQADAYVEKGIIDKEEAIRKRIYSSL 468
```



```
Sequence 90, Application US/10140274
Publication No. US20030143674A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C161
CURRENT APPLICATION NUMBER: US/10/140,274
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 90
LENGTH: 468
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-274-90
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```
Query Match          99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGWLIVLVLPPIQAFPPGSGDSKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP 60
DB 1 MGFLGTGWLIVLVLPPIQAFPPGSGDSKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP 60
QY 61 ENKPGQSNYSFVDNLNLRAITTEKEKTEKROSTIRSSPLDNKLNEVDVSTKNRKLIDY 120
DB 61 ENKPGQSNYSFVDNLNLRAITTEKEKTEKROSTIRSSPLDNKLNEVDVSTKNRKLIDY 120
QY 121 DSTSGDLHKFQDDPGDGLHLDGTPPLTAEDIVHKIARIYEENDRAVFDKIVSKLNLGL 180
DB 121 DSTSGDLHKFQDDPGDGLHLDGTPPLTAEDIVHKIARIYEENDRAVFDKIVSKLNLGL 180
QY 181 ITTESQAHTLEDEVAEVLQKLSKEANNYEEDPNKPTSWTENQAGKIPEKVTMAA10DGL 240
DB 181 ITTESQAHTLEDEVAEVLQKLSKEANNYEEDPNKPTSWTENQAGKIPEKVTMAA10DGL 240
QY 241 AKGENDETYSNTLTLTNGLERRTKTYSEDNFRFOYFPNFFALKSIDSEKEAKEKETLI 300
DB 241 AKGENDETYSNTLTLTNGLERRTKTYSEDNFRFOYFPNFFALKSIDSEKEAKEKETLI 300
QY 301 TIMKTLIDFYKMMVKYGTISPPEGVSYLENLDEMIALQTKNKLKNAATNISKLEPAPSE 360
DB 301 TIMKTLIDFYKMMVKYGTISPPEGVSYLENLDEMIALQTKNKLKNAATNISKLEPAPSE 360
QY 361 KSHETDSTKEEAAKMEKEVSLKDSKDNNSNGGKTDEPKGTETAYLEAIRKNIEWLK 420
DB 361 KSHETDSTKEEAAKMEKEVSLKDSKDNNSNGGKTDEPKGTETAYLEAIRKNIEWLK 420
QY 421 KHKKGKNEKEDYLSKMRDFTNKQADAYVEKGIIDKEEAFAIKRIYSSL 468
DB 421 KHKKGKNEKEDYLSKMRDFTNKQADAYVEKGIIDKEEAFAIKRIYSSL 468
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RESULT 8  
US-10-140-471-90  
Sequence 90, Application US/10140471

```
Publication No. US20030138887A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C163
CURRENT APPLICATION NUMBER: US/10/140,471
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 90
LENGTH: 468
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-471-90
```

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Query Match          99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGWLIVLVLPPIQAFPPGSGDSKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP 60
DB 1 MGFLGTGWLIVLVLPPIQAFPPGSGDSKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP 60
QY 61 ENKPGQSNYSFVDNLNLRAITTEKEKTEKROSTIRSSPLDNKLNEVDVSTKNRKLIDY 120
DB 61 ENKPGQSNYSFVDNLNLRAITTEKEKTEKROSTIRSSPLDNKLNEVDVSTKNRKLIDY 120
QY 121 DSTSGDLHKFQDDPGDGLHLDGTPPLTAEDIVHKIARIYEENDRAVFDKIVSKLNLGL 180
DB 121 DSTSGDLHKFQDDPGDGLHLDGTPPLTAEDIVHKIARIYEENDRAVFDKIVSKLNLGL 180
QY 181 ITTESQAHTLEDEVAEVLQKLSKEANNYEEDPNKPTSWTENQAGKIPEKVTMAA10DGL 240
DB 181 ITTESQAHTLEDEVAEVLQKLSKEANNYEEDPNKPTSWTENQAGKIPEKVTMAA10DGL 240
QY 241 AKGENDETYSNTLTLTNGLERRTKTYSEDNFRFOYFPNFFALKSIDSEKEAKEKETLI 300
DB 241 AKGENDETYSNTLTLTNGLERRTKTYSEDNFRFOYFPNFFALKSIDSEKEAKEKETLI 300
QY 301 TIMKTLIDFYKMMVKYGTISPPEGVSYLENLDEMIALQTKNKLKNAATNISKLEPAPSE 360
DB 301 TIMKTLIDFYKMMVKYGTISPPEGVSYLENLDEMIALQTKNKLKNAATNISKLEPAPSE 360
QY 361 KSHETDSTKEEAAKMEKEVSLKDSKDNNSNGGKTDEPKGTETAYLEAIRKNIEWLK 420
DB 361 KSHETDSTKEEAAKMEKEVSLKDSKDNNSNGGKTDEPKGTETAYLEAIRKNIEWLK 420
QY 421 KHKKGKNEKEDYLSKMRDFTNKQADAYVEKGIIDKEEAFAIKRIYSSL 468
DB 421 KHKKGKNEKEDYLSKMRDFTNKQADAYVEKGIIDKEEAFAIKRIYSSL 468
```

RESULT 9  
US-10-140-807-90  
Sequence 90, Application US/10140807  
Publication No. US20030134354A1

```

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Defoige, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C179
CURRENT APPLICATION NUMBER: US/10/140,922
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 90
LENGTH: 468
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-922-90

```

```

Best Local Similarity  99.1%;  Pred. No. 1,2e-152;
Matches  464;  Conservative  2;  Mismatches  2;  Indels  0;  Gaps  0;

```

Db	1	MGFLGTGWLIVLVLP	IOAFPPKPGSGQSK	LHNREL	SERPLENQ	IAEAEEDK	IKKTYPP	60		
QY	61	ENKGGGNSY	SVNDNLNLRAT	TEKEKTE	KEKQSR	SRSSPLDK	LNVEVDSTKRNKLDDY	120		
Db	61	ENKGGGNSY	SVNDNLNLRAT	TEKEKTE	KEKQSR	SRSSPLDK	LNVEVDSTKRNKLDDY	120		
QY	121	DSTRSGLDHKE	FQDDPDGLHOLDG	PLTAEID	IVHK	IAARIYE	ENDRAVEDKIVSKLNLGL	180		
Db	121	DSTRSGLDHKE	FQDDPDGLHOLDG	PLTAEID	IVHK	IAARIYE	ENDRAVEDKIVSKLNLGL	180		
QY	181	ITESQAHTLE	DEVAEVLQK	LKSIR	EANN	VEEDPNK	PTSWTENQAK	IPBKVTPMA	240	
Db	181	ITESQAHTLE	DEVAEVLQK	LKSIR	EANN	VEEDPNK	PTSWTENQAK	IPBKVTPMA	240	
QY	241	AKGNDENV	STLTLTNG	LERRRTYS	EDNFRD	QYFNP	FALLKSIDSEKAEKE	ETLI	300	
Db	241	AKGNDENV	STLTLTNG	LERRRTYS	EDNFRD	QYFNP	FALLKSIDSEKAEKE	ETLI	300	
QY	301	TIMKTLID	FEKMMVYGT	ISEBEG	SVYLEN	DEMIALQ	TKNKLEK	NATDNISK	LEPASE	360
Db	301	TIMKTLID	FEKMMVYGT	ISEBEG	SVYLEN	DEMIALQ	TKNKLEK	NATDNISK	LEPASE	360
QY	361	KSHEETST	STKEPAKME	KEKYS	LKSTK	DDNSNG	GKTDEK	GKTEAL	IAIRKNIEWLK	420
Db	361	KSHEETST	STKEPAKME	KEKYS	LKSTK	DDNSNG	GKTDEK	GKTEAL	IAIRKNIEWLK	420
QY	421	KHKDKGK	KEDYDLSK	MRDFT	INKQAD	AVEYK	ITLKE	EAAL	IKRITSSL	468
Db	421	KHKDKGK	KEDYDLSK	MRDFT	INKQAD	AVEYK	ITLKE	EAAL	IKRITSSL	468

```

RESULT 11
US-10-140-924-90
; Sequence 90, Application US/10140922
; Publication No. US20030134355A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

```

```

; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C17
; CURRENT APPLICATION NUMBER: US/10/140,924
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 90
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Saplen
US-10-140-924-90

Query Match          99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1,2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```

QY 1 MGFLGTGWIIVLVLPIDQAPKPGSQDLSLNHRELASRPPLNEQIAEAEEDKIKKTYPP 60
DB 1 MGFLGTGWIIVLVLPIDQAPKPGSQDLSLNHRELASRPPLNEQIAEAEEDKIKKTYPP 60
QY 61 ENKPGQSNYSFVDNLNLRAITEKEKIEROSIRSSPLDNKLNVEDVSTKNRKLIDY 120
DB 61 ENKPGQSNYSFVDNLNLRAITEKEKIEROSIRSSPLDNKLNVEDVSTKNRKLIDY 120
QY 121 DSTSGDLHKFQDDPDGHLQDGTPLTADYIYHKAARIYEENDRAVDFKYSKLNIGL 180
DB 121 DSTSGDLHKFQDDPDGHLQDGTPLTADYIYHKAARIYEENDRAVDFKYSKLNIGL 180
QY 121 ITESQAHTEDEVAEVLQKLISKEANNYEEDNPKPTSWENQAGKIPKVTMPAAIÖDGL 240
DB 181 ITESQAHTEDEVAEVLQKLISKEANNYEEDNPKPTSWENQAGKIPKVTMPAAIÖDGL 240
QY 241 AKGENDETYSNTLTLTNGLERRTKTYSEDNFRDFOYFPNFYALKSIDSEKAEKETLI 300
DB 241 AKGENDETYSNTLTLTNGLERRTKTYSEDNFRDFOYFPNFYALKSIDSEKAEKETLI 300
QY 301 TIMKTLIDFVKMMVKYGTISPEEGVSYLENDEMAIALQTKNLEKNATDNISKLPAPSE 360
DB 301 TIMKTLIDFVKMMVKYGTISPEEGVSYLENDEMAIALQTKNLEKNATDNISKLPAPSE 360
QY 361 KSHETDSTKEEAAKMEKEYGSLKSDTKDONSNGKTEDEPKGTAEATLEAIRKNIEWLK 420
DB 361 KSHETDSTKEEAAKMEKEYGSLKSDTKDONSNGKTEDEPKGTAEATLEAIRKNIEWLK 420
QY 421 KHKDKGNKEDYDLSKMRDFINKQADAYVEKGIIDKEEAIAIKRIYSSL 468
DB 421 KHKDKGNKEDYDLSKMRDFINKQADAYVEKGIIDKEEAIAIKRIYSSL 468
```

```

RESULT 12
US-10-140-926-90
; Sequence 90, Application US/10140926
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
```

```

; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C187
; CURRENT APPLICATION NUMBER: US/10/140,926
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 90
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Saplen
US-10-140-926-90

Query Match          99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1,2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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```

QY 1 MGFLGTGWIIVLVLPIDQAPKPGSQDLSLNHRELASRPPLNEQIAEAEEDKIKKTYPP 60
DB 1 MGFLGTGWIIVLVLPIDQAPKPGSQDLSLNHRELASRPPLNEQIAEAEEDKIKKTYPP 60
QY 61 ENKPGQSNYSFVDNLNLRAITEKEKIEROSIRSSPLDNKLNVEDVSTKNRKLIDY 120
DB 61 ENKPGQSNYSFVDNLNLRAITEKEKIEROSIRSSPLDNKLNVEDVSTKNRKLIDY 120
QY 121 DSTSGDLHKFQDDPDGHLQDGTPLTADYIYHKAARIYEENDRAVDFKYSKLNIGL 180
DB 121 DSTSGDLHKFQDDPDGHLQDGTPLTADYIYHKAARIYEENDRAVDFKYSKLNIGL 180
QY 181 ITESQAHTEDEVAEVLQKLISKEANNYEEDNPKPTSWENQAGKIPKVTMPAAIÖDGL 240
DB 181 ITESQAHTEDEVAEVLQKLISKEANNYEEDNPKPTSWENQAGKIPKVTMPAAIÖDGL 240
QY 241 AKGENDETYSNTLTLTNGLERRTKTYSEDNFRDFOYFPNFYALKSIDSEKAEKETLI 300
DB 241 AKGENDETYSNTLTLTNGLERRTKTYSEDNFRDFOYFPNFYALKSIDSEKAEKETLI 300
QY 301 TIMKTLIDFVKMMVKYGTISPEEGVSYLENDEMAIALQTKNLEKNATDNISKLPAPSE 360
DB 301 TIMKTLIDFVKMMVKYGTISPEEGVSYLENDEMAIALQTKNLEKNATDNISKLPAPSE 360
QY 361 KSHETDSTKEEAAKMEKEYGSLKSDTKDONSNGKTEDEPKGTAEATLEAIRKNIEWLK 420
DB 361 KSHETDSTKEEAAKMEKEYGSLKSDTKDONSNGKTEDEPKGTAEATLEAIRKNIEWLK 420
QY 421 KHKDKGNKEDYDLSKMRDFINKQADAYVEKGIIDKEEAIAIKRIYSSL 468
DB 421 KHKDKGNKEDYDLSKMRDFINKQADAYVEKGIIDKEEAIAIKRIYSSL 468
```

```

RESULT 13
US-10-141-698-90
; Sequence 90, Application US/10141698
; Publication No. US20030134357A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
```

RESULT 14  
US-10-141-702-90  
: Sequence 90, Application US/101411702  
: Publication No. US20030134358A1  
: GENERAL INFORMATION:  
: :  
: APPLICANT: Baker, Kevin P.  
: APPLICANT: Besselin, Maureen  
: APPLICANT: DeForge, Laura  
: APPLICANT: Desnoyers, Luc

RESULT 15  
US-10-141-704-90  
Sequence 90, Application US/10141704  
Publication No. US2003013459A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bergesini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C209  
CURRENT APPLICATION NUMBER: US/10/141,704  
CURRENT FILING DATE: 2002-05-08  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 90  
LENGTH: 468  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-141-704-90

Query Match 99.3%; Score 2384; DB 12; Length 468;  
Best Local Similarity 99.1%; Pred. No. 1.2e-152;  
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGWIIVLVLPPIAFKPGSGQSKLHNRLSAPRLNEQIAEAEDKIKKTYPP 60  
DB 1 MGFLGTGWIIVLVLPPIAFKPGSGQSKLHNRLSAPRLNEQIAEAEDKIKKTYPP 60  
QY 61 ENKPGQSNYSFVDNLNLRAITTEKEKIKEROSIRSSPLDNKLNEVDVSTKNRLLDDY 120  
DB 61 ENKPGQSNYSFVDNLNLRAITTEKEKIKEROSIRSSPLDNKLNEVDVSTKNRLLDDY 120  
QY 121 DSTSGDLHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYENDRAVFDKIVSKLNLGL 180  
DB 121 DSTSGDLHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYENDRAVFDKIVSKLNLGL 180  
QY 181 ITESQAHLEDEVAEVLQKLSKEANNYEEDPNKPTSWENQAGKIPKVTPMALDGL 240  
DB 181 ITESQAHLEDEVAEVLQKLSKEANNYEEDPNKPTSWENQAGKIPKVTPMALDGL 240  
QY 241 AKGENDETVSNTLTLTNGLERRTKTYSEDNRFQYPPNFYALKSIDSEKAKEETLI 300  
DB 241 AKGENDETVSNTLTLTNGLERRTKTYSEDNRFQYPPNFYALKSIDSEKAKEETLI 300  
QY 301 TIMKTLDYFKMMYKGTISPEEGVSTLENDEMIALQTKNKLKNAATDNISKLEPAPSE 360  
DB 301 TIMKTLDYFKMMYKGTISPEEGVSTLENDEMIALQTKNKLKNAATDNISKLEPAPSE 360  
QY 361 KSHETDSTKEEAKMEKEVSLKSDTSDNSNPGKTDDEPKGTEAYLEAIRNTEMLK 420  
DB 361 KSHETDSTKEEAKMEKEVSLKSDTSDNSNPGKTDDEPKGTEAYLEAIRNTEMLK 420  
QY 421 KHKDKGKEDYDLSKMRDFTNKQADAVEKGIIDKEEAEAIKRIYSSL 468  
DB 421 KHKDKGKEDYDLSKMRDFTNKQADAVEKGIIDKEEAEAIKRIYSSL 468

Search completed: August 28, 2003, 10:31:55  
Job time : 61 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2003, 09:59:03 ; Search time 69 Seconds

(without alignments)  
1750.270 Million cell updates/sec

Title: US-09-554-945b-2

Perfect score: 2402  
Sequence: 1 MGFLGTGWTIVLVLPIDAF.....EKGIIDKEAEAKRIYSL 468

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2053	85.5	466	11	Q8RID7 mus musculus
2	1216	50.6	457	13	Q91847 xenopus lae
3	200	8.3	9210	5	Q9V7G8 drosophila
4	200	8.3	9270	5	Q8MID9 drosophila
5	197	8.2	2081	10	Q9LH98 arabidopsis
6	191	8.0	2139	5	Q07569 entamoeba h
7	188.5	7.8	2760	5	Q815Y2 plasmodium
8	187.5	7.8	1661	5	Q06166 plasmodium
9	183.5	7.6	1175	16	Q8XNM6 clostridium
10	183	7.6	1434	5	Q81492 plasmodium
11	182	7.6	951	5	Q096229 plasmodium
12	181	7.5	1790	3	Q07380 saccharomyc
13	180.5	7.5	3504	5	Q81L45 plasmodium
14	180	7.5	1871	10	Q9SRD5 arabidopsis
15	179.5	7.5	853	10	Q9LFE4 arabidopsis
16	178.5	7.4	1263	5	Q81K49 plasmodium

17	178.5	7.4	1964	5	Q85W07	Q85W07 lolligo peal
18	177.5	7.4	682	5	Q81BV6	Q81BV6 plasmodium
19	175	7.3	10578	5	Q81SE5	Q81SE5 caenorhabdi
20	175	7.3	18519	5	Q81SE6	Q81SE6 caenorhabdi
21	175	7.3	18534	5	Q81SE7	Q81SE7 caenorhabdi
22	174.5	7.3	1320	11	Q9JK25	Q9JK25 rattus norv
23	174.5	7.3	1323	5	Q9NB35	Q9NB35 plasmodium
24	174.5	7.3	1510	5	Q25920	Q25920 plasmodium
25	173	7.2	1358	5	Q096275	Q096275 plasmodium
26	173	7.2	1786	5	Q9U0P0	Q9U0P0 plasmodium
27	172.5	7.2	1979	5	Q096133	Q096133 plasmodium
28	172	7.2	493	5	Q25886	Q25886 plasmodium
29	171.5	7.1	1795	5	Q81E35	Q81E35 plasmodium
30	171.5	7.1	2612	5	Q815X5	Q815X5 plasmodium
31	171	7.1	734	5	Q95V49	Q95V49 drosophila
32	171	7.1	840	5	Q815X4	Q815X4 plasmodium
33	171	7.1	2269	5	Q26223	Q26223 plasmodium
34	171	7.1	2747	5	Q9BUX9	Q9BUX9 plasmodium
35	170.5	7.1	1596	5	Q81I44	Q81I44 plasmodium
36	169.5	7.1	1134	2	Q99051	Q99051 streptococ
37	169.5	7.1	1464	5	Q81IF6	Q81IF6 plasmodium
38	169	7.0	1909	5	Q25893	Q25893 plasmodium
39	169	7.0	3484	5	P91257	P91257 caenorhabdi
40	168	7.0	1272	16	Q98PR8	Q98PR8 mycoplasma
41	168	7.0	2006	5	Q81DI0	Q81DI0 plasmodium
42	168	7.0	2867	5	Q9N2M3	Q9N2M3 plasmodium
43	167.5	7.0	924	5	Q15738	Q15738 dictyosteli
44	167	7.0	1112	16	Q8EMQ1	Q8EMQ1 mycoplasma
45	167	7.0	2771	5	Q26216	Q26216 plasmodium

#### ALIGNMENTS

RESULT 1  
Q8RID7 PRELIMINARY: PRT: 466 AA.

AC Q8RID7;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Similar to secretogranin III.  
OS Mus musculus (mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SOURCE FROM N.A.  
RC TISSUE=Eye;  
RA Strausberg R.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC024785; AAH24785.1;  
SQ SEQUENCE 466 AA; 52783 MW; AB1CB9667276315C CRC64;

Query Match 85.5%; Score 2053; DB 11; Length 466;  
Best Local Similarity 86.6%; Pred. No. 5,8e-96;  
Matches 408; Conservative 17; Mismatches 38; Indels. 8; Gaps 2;

QY	1	MGFLGTGWTIVLVLPIDAFPPKPGSODKSLHNRELSAERPLNEQJAEAEEDIKRT	57
DB	1	MGFLGTGWTIVLVLPIDAFPPKPGSODKSLHNRELSAERPLNEQJAEAEADIKKA	60
QY	58	YPPENKPGQSNYSFVNILNLRAITEKEKEKERQSIKSSPLDNKLNVEDVSTKRRKI	117
DB	61	FPESKRPESNYSVONLNLRAITEKEKEKERQSIKSSPLDNKLNVEDVSTKRRKI	120
QY	118	DDYDSTKSGIDHKFGQDDPGLODGTPLTAEDIYVKAARIYEENDRAVFDKYSKLLN	177
DB	121	DEYDSTKSGIDHKFGQDDPGLODGTPLTAEDIYVKAARIYEENDRAVFDKYSKLLN	180
QY	178	LGITTSQAHTLEDEVAEALQKLSKEANNYEETLDPKPSRWPNQNGKIPKVTYPAALIO	237
DB	181	LGITTSQAHTLEDEVAEALQKLSKEANNYEETLDPKPSRWPNQNGKIPKVTYPAALVO	240

Db 348 PSEIDKNADESDSTREKAAXKEFEELIKDSTKPEPND - AAESKPCKATYILEAIKNKI 400

Oy 417 EMUKHKHKKNKEDDYDSKRBDLTINQADAYVEKGILDKKEAEAKIRIYSSL 468  
|||||:|:| | ||||| :|:|:|||||:||||| |||||

Db 406 EMLKENHKKNGDNDSLKLKLOVNOAADYVEKGLDKKEANVIKRIYSSL 457

RESULT 3

09VTG8 ID 09VTG8 PRELIMINARY; PRT: 7210 AA.

AC 09VTG8;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE CG18255 protein.

GN SRRN-Mlck OR CG8304 OR CG18255.

OS Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxId=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkely;

RX MEDLINE=20196006; PubMed=10731132;  
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
Rutledge J.C., Hughes M.O., Gillio M.P., White O., Frazer L.H.,  
Sutton G.G., Wortman J.R., Fendell M.D., Zhang Q., Chen L.X.,  
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,  
Abdill J.F., Adhyani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
Ballew R.M., Basu A.I., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,  
Botchan D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
Cherry J.M., Crawley S., Dahlke C., Davenport L.B., Davies P.,  
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
Foster C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,  
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeigwan C.,  
Jalili M., Kasust F., Kapran G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
Kimble B.E., Kodira C.D., Kraft C., Kravitz S., Kuyp D., Lai Z.,  
Lasko P., Lei Y., Levitsky A.A., Li J.Z., Li Z., Liang Y., Lin X.,  
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
Nelsson D.R., Nelson K.A., Nixon K., Nussekern D.R., Pacle J.M.,  
Palazzo M., Platan G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
Reichert K., Remington I., Saunders R.D.C., Scheeler F., Shen H.,  
Shen B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,  
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
Svirskas R., Tecor C., Turner R., Venter E., Wang A.H., Wang X.,  
Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,"  
The genome sequence of Drosophila melanogaster."

RL [2]  
SCIENCE 287:2185-2195(2000).

RP SEQUENCE FROM N.A.  
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
Barzon J., An H., Baldwin D., Barzon J., Beeson K.Y., Busam D.A.,  
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
Dorsett K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
Ferrera S., Frishe E., Galie R.F., Gang N.S., George R.A.,  
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
Ibeigwan C., Jalili M., Kruse D., Li P., Mattei B., Mochlyeff I.,  
Mortrud M.T., Nelson D.R., Nelson K.A., Nixon K., Palocz J.M.,  
Palazzo M., Platan G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
Reichert K., Remington I., Saunders R.D.C., Scheeler F., Shen H.,  
Shen B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,  
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
Svirskas R., Tecor C., Turner R., Venter E., Wang A.H., Wang X.,  
Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,"  
The genome sequence of Drosophila melanogaster."



RA Stapleton M., Strong R., Svirska R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RT "Sequencing of *Drosophila melanogaster* genome."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E.,  
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutniak P., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RT "Annotation of *Drosophila melanogaster* genome."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Flybase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: A6003808; AAM70936.1; -  
 DR Flybase: FBgn013988; Strn-M1C.  
 DR InterPro: IPR003961; FN-III.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003598; Ig-C2.  
 DR InterPro: IPR003006; Ig-MHC.  
 DR InterPro: IPR003596; Ig-V.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR002290; Ser\_thr\_kinase.  
 DR InterPro: IPR001245; Tyr\_kinase.  
 DR Pfam: PF00041; fn3; 2.  
 DR Pfam: PF00047; Ig; 29.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Prodom: P000001; Prot\_kinase; 1.  
 DR SMART: SM00408; Igc2; 29.  
 DR SMART: SM00406; Igv; 4.  
 DR SMART: SM00220; S-TC; 1.  
 DR SMART: SM00219; Tyrc; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 26.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR ATP-binding; Immunoglobulin domain; Transferase.  
 SQ SEQUENCE 9270 AA; 1036749 MW; 0DD82D040B27C2AD CRC64;

Query Match 8.3%; Score 200; DB 5; Length 9270;  
 Best Local Similarity 23.8%; Pred. No. 0.42;  
 Matches 110; Conservative 83; Mismatches 180; Indels 90; Gaps 19;

QY 35 ELASERPLNEQIAEEDKIKKTYPPENKPGOSNYSPVONLNLRAITEKEIEKEROSI 94  
 Db 4757 EIVSKIRIDEKAQESQKEVGS---EAKPKAKV-----LEKKSIEEKELEKKEQ 4806  
 QY 95 RSPSLDNKLVNEDVSTNRRLID--YDSTKSGIDHKFODDPDGLHQLDGTPLTAEDIV 152  
 Db 4807 TESAIIDEKSQAEEVSEIKITDEKAQESQKEVGS-EAKPKAKVLEKKSIEEKE 4865  
 QY 153 HK-----IAARIYEENDRAVFPDKIVSKLNLGLITSQAHTEDEVAEVLQ-KLISKEANN 207  
 Db 4866 NKKEKQTESAIDEKSQAEEVSEIKITDEKAQESQKEVGS-EAKPKAKVLEKKSIE 4925  
 QY 208 YEEDPNKPTSWTENQAKIPEKVTMAIOTDLAKGENDEVSNLTLTNGLEERTKTY 267  
 Db 4926 EEKLEDKKEKTE-----SAIDKFKQAEVSEIVSEKIT-----DEKAESR 4967  
 QY 268 EDNFRDFQYPPNFYALL--KSIDSEK--EAKKET-----LITIMKTLID-- 308  
 Db 4968 KEEVKDSEAKPKKAKVLEKKSIEEKELEKKEKQTESAIDEKSQAEEVSEIVSEKITDEK 5027

QY 309 ---FVKMKVXYGTISP-----EEGVSYLENLDEMIALQTKNLEKNATNISKLPAPS 359  
 Db 5028 AQESQKEVNDSEAKPKKAKVLEKKSIEEKELEKKEKQITKY---ATDKSQVEVSE 5084  
 QY 360 EKSHEETSTKEEAKMEKEVSLKSDTSDNSNPGKTDPEKPGTEVALEAIRKNLEWL 419  
 Db 5085 IVEKISIEEKAEEESQKVE-----LKDS-----EAKSKAKVLEKKSIEEKE 5126  
 QY 420 KKHKKKKKKEDYDLSKMRDPLNKADAVKEGILDKEEAEK 462  
 Db 5127 DENDKK-QKEGATNKSQK-AEADAVPEK--ISEEKVAEIK 5164

RESULT 5  
 Q9LH98 PRELIMINARY; PRT; 2081 AA.  
 AC Q9LH98;  
 DT 01-OCR-2000 (Tremblrel, 15, Created)  
 DT 01-OCR-2000 (Tremblrel, 15, Last sequence update)  
 DT 01-OCR-2002 (Tremblrel, 22, Last annotation update)  
 DE Genomic DNA, chromosome 3, BAC clone: T19N8.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 ON NCBI\_Taxid=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-Columbia;  
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Columbia;  
 RX MEDLINE=20363099; PubMed=10907853;  
 RA Nakamura Y.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.  
 RT Sequence features of the regions of 4,251,695 bp covered by miniseq p1,  
 RT TAC and BAC clones."  
 RL DNA Res. 7:217-221(2000).  
 DR EMBL: AP002057; BAB03174.1; -  
 SQ SEQUENCE 2081 AA; 232851 MW; D3603E1F85EFF729 CRC64;

Query Match 8.2%; Score 197; DB 10; Length 2081;  
 Best Local Similarity 25.2%; Pred. No. 0.1;  
 Matches 120; Conservative 68; Mismatches 175; Indels 114; Gaps 21;

QY 27 QDKSLHNRSLASERPLNEQIAEED-----KIKKTYPPENKPGOSNY 70  
 Db 707 EDKLEENKESQYDSKDDKSVDDKQEBQAIYGGESKDDKSVKAKKKESKENKTKTNEN 766  
 QY 71 FVDNL--NLRAITEKEKIE--EROSINSSPLDNKLVNEDVSTNRRLIDYDSTKSG 126  
 Db 767 RVRNKEENVQKKKSEKKEKESKDAKSVEYKDN-KKLSSTENR---DEAKERSG 821  
 QY 127 IDHKFODDPDGLHQLDGTPLTAEDIVHKIAARIYEEN--DRAVEDKIVSKLNLGLITE 183  
 Db 822 EDNKEDKESKDY-----SVEAKEKNENGVNDVNGKEDSKDLKDRSYE 868  
 QY 184 SOAHLEED-----EVAEVLQKLSKE---ANNYEDPKKPTSWTENQAKIPEKVTMA 234  
 Db 869 VYANKKEESKKKREEVORNDKSTKEVRDFANNMIDYQKSG--ESVYKKKDEK----- 921  
 QY 235 AIQDGLAGGENDETYSNTLTNGLEERTKTYSEDNFRQYGFPPNFYALLKSIDSEKAK 294  
 Db 922 --KEG-NKEENKDTI--NTSSKQKQDKKKKESKN-----SNMKKEED 962  
 QY 295 EKETLITIMKTLIDFVKMKVXYGTISP EGVSYLENLDEMIALQTKNLEKNATNISKL 354  
 Db 963 KKEYVNNELKQEDKKETTSKNSKLK-----ENKD-----NKKEKSEDSASK- 1008  
 QY 355 FPAPEKSHETDS--TKEDAAKMEKEVSLKSDTSDNSNPG-----GKIDE 400

DB 1009 --NREKXEKSKTKEBAKKEKKSQDKRREKDEBKRKSKKEKESRDLKAKKEE 1066  
QY 401 PKGTAYLEAIRKNIEMLKHKDKGNKRDYDLKSMRDFINQAOAYVEKGLDKRE 457  
DB 1067 TEKRES-----ENHKSRRKDEKKEHEDNKSMMKEED--KKEKKHESKSKRKE 1115

## RESULT 6

007569 PRELIMINARY; PRT: 2139 AA.

AC 007569; 002504;  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)  
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)  
DE Myosin heavy chain.  
GN MYCA.  
OS Entamoeba histolytica.  
OC Eukaryota; Entamoebidae; Entamoeba.  
OX NCBI\_TaxId=5759;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-HMI:IMSS;  
RX MEDLINE=93295430; PubMed=8515774;  
RA Raymond-Denise A., Sansonetti P., Guillen N.;  
RT "Identification and characterization of a myosin heavy chain gene (mhca) from the human parasitic pathogen Entamoeba histolytica";  
RT Mol. Biochem. Parasitol. 59:123-131(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-HMI:IMSS;  
RX Gullien N.;  
RA Gullien N.;  
RT Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.  
DR EMBL: L03534; AAB48065.1; -.  
DR HSSP: P08799; IMND.  
DR InterPro: IPR000048; IQ\_region.  
DR InterPro: IPR001609; myosin\_head.  
DR Pfam: PF00612; IQ\_2.  
DR Pfam: PF00063; myosin\_head; 1.  
DR PRINTS: PR00193; MYOSINHEAVY.  
DR ProDom: PD000355; myosin\_head; 1.  
DR SMART: SM00242; MYSC; 1.  
SQ SEQUENCE 2139 AA; 245225 MW; C68307341DB51DD1 CRC64;

Query Match 8.0%; Score 191; DB 5; Length 2139;  
Best Local Similarity 20.8%; Pred. No. 0.21;  
Matches 106; Conservative 107; Mismatches 193; Indels 104; Gaps 23;

QY 20 FPKPGSQDLSLHRELAEPRPLNQIAEEDKIKTKYPPEN-----KPGQSNYSFV 72  
DB 85 FEEBGRKKDKLEID-----LKKKLA-----EIKKRAENALASATAKGELEAKIQ 906  
QY 73 D-----NNLRAITEKEKIEKERSIRSSPLDNKLNVEDVD- 109  
DB 907 DLEDKISELESKLSAELEDKQELNLEKIEMLLEEDKEKLETDNLKDLKDSKLGEDLV 966  
QY 110 -----STKNRLIDVDYSTKGLDHPDDPGLHQLDGTPLTADYHAKTIARY 160  
DB 967 EITELNSQINTLN-ATVDRKDKTIAEMQESIDEKEDETKLKGDIKLEEKDDI----- 1020  
QY 161 EENDR-----AVFDKIVSKLNLGLITESQAHTLEDEVAEVLQKLSKEANNYEEDNPKT 216  
DB 1021 -EQDADVYSATKDDIADKAKLNTIT---ECEDAKDEIAKLEBLEEE--NNKKDLTNEL 1073  
QY 217 SKTENQAGKIPKVTYPMAL-----ODGLAKG--ENDETVSNLTLLNG--LERRTKYS 267  
DB 1074 QOTOLKLGTEKSLAOVNATKASDERDPLTSQNLNENKLTITKNTKADLEKKSIGLK 1133  
QY 268 EENFDEFOYFPNFYALKSID-----SEKAKEKELLIMKTLIDFV--KMWVKYGTISP 321  
DB 1134 QD-YEDLEDDKN-----KIBGDLRNAOKIKELDELTGKADVSOYLQKQEEY----- 1181  
QY 322 EBGVSLYENLDEMIALQTKNLEKNAVDNISLFPAPSEKSEETDSTEEAK---ME 377

DB 1182 ESQIAKQOEKBAIGNDVKNK-EKTIKE--KELEIQLQEKIDETFEVEKEDAKKKKEIE 1238  
QY 378 KEYSLSKSDTKDONSFGKGTDEPKGTAYLEAIRKNIEMLKHKDKGNKRDYDL-SKM 436  
DB 1239 KEKALQOE-KENVESSKNSKTERDKKRLDNDKDTQKLDMDTADNEKLAKADLEAQL 1297  
QY 437 RDEINKQADAYVEKGLDKEEAFAIKRYS 466  
DB 1298 NEYQDNHEKAVADAEILNKKKAOSDKELNS 1327

## RESULT 7

0815Y2 PRELIMINARY; PRT: 2760 AA.

AC 0815Y2;  
DT 01-MAR-2003 (TREMblrel. 23, Created)  
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)  
DE Hypothetical protein.  
GN PFL0315C.  
OS Plasmodium falciparum (isolate 3D7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxId=36329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=3D7;  
RX MEDLINE=22255705; PubMed=12368864;  
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,  
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,  
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,  
RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angioli S.,  
RA Perlea M., Allen J., Selengut J., Haft D., Mather M.W., Valiya A.B.,  
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,  
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,  
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,  
RA Fraser C.M., Barrell B.;  
RT "Genome sequence of the human malaria parasite Plasmodium falciparum";  
RT Nature 419:498-511(2002).  
DR EMBL: AE014845; AAN36152.1; -.  
DR Hypothetical protein.  
SQ SEQUENCE 2760 AA; 330896 MW; EE964C4845181AC CRC64;

Query Match 7.8%; Score 188.5; DB 5; Length 2760;  
Best Local Similarity 20.7%; Pred. No. 0.38;  
Matches 119; Conservative 97; Mismatches 203; Indels 155; Gaps 24;

QY 29 KSLHNRLELSAERPLNQIAEEDKIKTKYPPEN-----DKIKTYPPENKPGQSNYSFV 73  
DB 1452 KNEAKEEETERNINDQVNERKEMDVNSKNERELIYOYHNEINTNNKEEGKKNLK 1511  
QY 74 NNL--LLRAITEKEKIEKERO--SIRSSPLDNKLNVEDYSTKNRLIDVDYSTKGLDH 129  
DB 1512 EINDCLNDYINQKKKKKKNNMAMYGRIYKRONNRNINIKNDLKITSKSESEGFNDY 1571  
QY 130 KF-----QDDPGLHQLDGTPLTA--DIVH-----KIARIYEEN-- 163  
DB 1572 AFYAERFFEVITGYNSEPDYLSIDQAKNEKNKDIHNNNIKISKMKKENTYENSPF 1631  
QY 164 ---DRAVPD-----KIVSKLNLGLITESQ----- 186  
DB 1632 HNYGRIRYKSKSNPNYKIKISTHINALKKRKKTKLKSISINFTMNSNNKIYKR 1691  
QY 187 -----HTLEDEVAEVLQKLSKEANNYEDP-----NKPTSWTENQAK 225  
DB 1692 TSIKNNTIDYNNNSTITKTIHKQON--VEDQGYIDLKTRKRLIYDALDINOOTOOKNLK 1749  
QY 226 IPEKTYPMALQDGLAKGENDETVSNLTLLNG--LERRTKYSEDNFPDPYFPNFYAL 283  
DB 1750 ITENTT-----QVGKKHGON---VSNITKNTAMLEKTKRKGNDNEED-----QFSBE 1796  
QY 284 LKSIDSEKAKEKELLITIMKTL-IDFVMMWKYGTISPSEGVSLYENLDEM----- 334

Db 1797 LKALEKIKLKELEK-IEELKTLEEEKKRLLEELNSLKVEEKKKKNNMEKKMEEMK 1855  
 QY 335 IALQTKNLEK-----NATDNISKL-----FPAPSKSHEPDSTEEAKM--EKE 379  
 Db 1856 IELQRRKEEEKLLQYRROEQIRKLELKKKEELKLEEMNKLEORRKEEIKKKEEKE 1915  
 QY 380 YGSLKSTYDSDNSNGKTDPEPGKTEAYL-----EAIRKNIE--WLKKHDKGNKED 430  
 Db 1916 REKLKKIKKQOQKEEKKQEOQRKKQIKLMEEMKRFEEQRRKKVELKWLKEEKKRDELK 1975  
 QY 431 YOLSKMRDFINKQADAVYKGLDKLEEAIRRI 464  
 Db 1976 LEOQKKRE-ERKKMEEEKKREKKREKKM 2008

## RESULT 8

Q06166 PRELIMINARY: PRT: 1661 AA.  
 ID 006166  
 AC 006166  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, last annotation update)  
 DE Mature PARASITE-Infected erythrocyte surface antigen (Antigenic protein PfEMP2).  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PALO ALTO;  
 RX MEDLINE=92158014; PubMed=1741020;  
 RA Coppel R.L.;  
 RT "Repeat structures in a Plasmodium falciparum protein (MESA) that binds human erythrocyte protein 4.1.";  
 RL Mol. Biochem. Parasitol. 50:335-347(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PALO ALTO.  
 RX Kun J.F.J., Waller K.L., Coppel R.L.;  
 RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 797-850 FROM N.A.  
 RX MEDLINE=93122844; PubMed=1478701;  
 RA Saul A., Yeganeh F., Howard R.J.;  
 RT "Conservation of repeating structures in the PfEMP2/MESA protein of Plasmodium falciparum.";  
 RL Immunol. Cell Biol. 70:353-355(1992).  
 DR EMBL; AF056936; AAC13303.1;  
 DR EMBL; S52458; AAB24869.1;  
 DR InterPro: IPR001623; DnaJ\_N.  
 DR Pfam: PF00226; DnaJ\_1.  
 DR SMART: SM00271; DnaJ\_1.  
 DR PROSITE: PS50076; DnaJ\_2; 1.  
 DR Antigen.  
 SQ SEQUENCE 1661 AA; 195479 MW; AF340527D85A9D29 CRC64.

Query Match 7.8%; Score 187.5; DB 5; Length 1661;  
 Best Local Similarity 19.3%; Pred. No. 0.23;  
 Matches 91; Conservative 91; Mismatches 191; Indels 99; Gaps 14;

QY 22 KPGSOPKSLHNEELSAERLNLQIAEEDTKIKTTPPENKPGQSNYSFVNDLNLRAI 81  
 Db 895 KQANAKDKLEIQEKEKEVEKKEVEKKEVEKKEVEKKEVEKKEVEKKEVEKKEVEK 937  
 QY 82 TEKEITEKEROSIRSSPLDNKLNVEDVSTKRNKRLIDYDSTKSGLDHKFODDPDGLHOL 141  
 Db 938 KEKEVEKKEVEKKEVEKKEVEKKEVEKKEVEKKEVEKKEVEKKEVEKKEVEKKEVEK 996  
 QY 142 DGPPLAEDIVHIAIRIYEN-----DRAVFDKIVSKLNLGLITESQAHTLEDEVAE 195  
 Db 997 IGGELIIEETKEKVRKVRKRNKNKNKNDVIVQEIIMNEMLRKRDYANKDKVIEQEKKEE 1056  
 QY 196 VLQKLSKANNNEEDPNKPTSWTENQACKIPEKIVPMAIQQDLAKGENDEVSTLT 255

Db 1057 VKEKEVEKKEVEKKEE-----VKEEVEKEDT----- 1086  
 QY 256 TNGLERRRTKYSSEDFRFOYFPNFPYALNKSIDSEKAEKET-----LITMKTLIDFVK 311  
 Db 1087 -----ESKKEIEQE-----KKKEVEKKEVEDTENKOKVIGQELIIEIK 1127  
 QY 312 MMVYGTISPEGVSYLENDEMIALQTKN-LKRNATDNISKLFPAPSKSH-EETDST 369  
 Db 1128 KEVKRRV---KRRNNKNKNKNDVIVQEIIMNEVDNEDVNEKTPANKDKVIEQEKKEVEKKEE 1184  
 QY 370 KEAAKMEKEVSGSLKDS-----TKDSDNSNPGKTDPEPGKT---EAYLEAIRKN 415  
 Db 1185 KEKEVEKKEVEKEDTISKKEIEQEKKEVEKKEVEKEDTENKDKVIGQELIIEIKKE 1244  
 QY 416 IE--WLKKHDKGNKEDYDLSK-MRDFINKQADAVYKGLDKLEEAIRRI 464  
 Db 1245 VKRRVKKRNKNKNKNDVIVQEIIMNEVDNEDVNEKTPANKDKVIEQEKKEVEK 1296

## RESULT 9

Q08XNW6 PRELIMINARY: PRT: 1175 AA.  
 ID 08XNW6  
 AC 08XNW6  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)  
 DE Probable exonuclease.  
 GN SBCC OR CPE0216.  
 OS Clostridium perfringens.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1502;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=13 / Type A;  
 RX PubMed=11792842;  
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,  
 RA Shiba T., Ogasawara N., Hattori M., Kihara S., Hayashi H.;  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 DR EMBL; AP003185; BAB79922.1;  
 DR InterPro: IPR003439; ABC\_transporter.  
 DR Exonuclease: Complete proteome.  
 SQ SEQUENCE 1175 AA; 136878 MW; 7C6D2366525019C1 CRC64;

Query Match 7.6%; Score 183.5; DB 16; Length 1175;  
 Best Local Similarity 21.5%; Pred. No. 0.25;  
 Matches 112; Conservative 86; Mismatches 190; Indels 133; Gaps 21;

QY 29 KSLHNEELSAERLNLQIAEEDTKIKTTPPENKPGQSNYSFVNDL-NLRAITEKE-- 85  
 Db 256 KELYDRRIEIE-----SLVRSSEIKSFKEVEISNKAQVIVFINNLEELIKKEINKEDLK 311  
 QY 86 -KIEKERSIRSSPLDNKLNVEDVSTKRNKRLIDYDSTKSGLDHKFODDPDGLHODG 143  
 Db 312 FSLNKKKLEELNLNRENKLEKFEFTKKKEELPLRLKKEKLES--QKEDILLQJKA 369  
 QY 144 TPPLTIEDIVHKT-----AARIYENDRAVFDKIYSK-----LNLWG 179  
 Db 370 DGVKLKEACKKIFEDRSKCDTKLNSIEVEKRLNELKEKEKREKELFVHEEFKNKINS 429  
 QY 180 LITESQAHTLEDEVAEVLQKL--SKANNNEEDPNKPTSWTENQAGIPEKIVPMAIQ 237  
 Db 430 LFTLNSYESLDKQFNEIKSEVEIKRYIKNLTEDEKSEK-----DLKQVESLSKIR 482  
 QY 238 DGLAR-----GENDETYSNTLTLNGLERRTKYSSEDFRFOYFP 278  
 Db 483 DKLESLEKETPDSDSILEKQIKGIEYREKLNKRYEIKNSLEBSIKTN-----531  
 QY 279 NFVALKSIDSEKAEKETLITMKTLIDFVK-----MVYGTISPEGVSYL 328

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Db 532 NFEKLTKEENKLTLEKE--VRELKDYINKVVEELAKLRENLVE-GECCPVCSTHH 588
Qy 329 E-----NIDE-----MIALQTKNLEKNAIDNISKL---FPAPSEK-----SHEETDS 368
Db 589 ELNKVERKINLEESNEKTITLESKEKLELLEFSKIEATLEXYENKRIEELNISIEVGE 648
Qy 369 TKEEAK-MEKEXGSLKSDTSDNSNPGKTDPEKGTKEAYLEAIRNIEMLKHKGN 427
Db 649 VNEERLKFLEEFENITLKDKEENLKK-----ENLEKLEKL--EKKNN 651
Qy 428 KEDYDLSKMDPINKQADAVVEKGLDKKEAEAIKRIYSSL 468
Db 692 LE-----NIFNKAEVILCEKIVREKEIASIKELDKEL 724

RESULT 10
ID 081492 PRELIMINARY; PRT; 1434 AA.
AC 081492;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE Mature parasite-infected erythrocyte surface antigen (MESA) or
DE PFEMP2.
GN MESA..
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
RA Hall N., Bowman S., Churcher C., Quail M., Barrett B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=22255708; PubMed=12368867;
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Latke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajadream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrett B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."
RL Nature 419:327-531(2002).
DR EMBL:AL929351; CAD51374.1;
SQ SEQUENCE 1434 AA; 168287 MW; AB0005F9DC26C989 CRC64;

Query Match 7.6%; Score 183; DB 5; Length 1434;
Best Local Similarity 20.7%; Pred. No. 0.33;
Matches 99; Conservative 98; Mismatches 180; Indels 102; Gaps 23;
Qy 27 QDKSLNRELISAERPLNEQ-----IAEAEDKIKKTYPPENKPGQSNYSFVDMNLRLAI 81
Db 501 KDKVLGEDEKEDKKNDEKDKVLGEDEKEDK-----EKNQCKAD-KYIGSEKQKEI 554
Qy 82 TEKEKTEKE-----KOSINSSPLDNKLNVEDVSTNRKLLIDYDSTKSLDHRKFD-- 133
Db 555 --KEVEKRYKKKKKKKKKKGIGKEN--DEGNDKVGKPEII--IEVEKEIKROVEDGK 608
Qy 134 --DPDGLHQLDGPFLAEDIVHKIARIYE--ENDRAVVDKIVSKLNLGLITTESQART 188
Db 609 ENTEGNDKVGKPEIITEVEKEIKROVEDGKEDKVGKGP--EITTEVEKEE 664
Qy 189 LEDEVAEVLQ-----KLISKANNYEEDPNKPTSWTENQAGKIPEKVTPMALQDGL 240

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Db 665 IKKQVEGIGKENDESKDKIGOEIITEVEKESIKENDIENK-----DKVIGOEIITEEV 719
Qy 241 AKG--ENDETVSNLTTLTJNGLERRTYSEDNFRDPYPPNVALKSIDSEKAEKET 298
Db 720 KEGIKEND-----TENKDKVIGOEIITE-----EVKKEIKOKEGKNKEN 759
Qy 299 LITL-----MKTLLDPVKMKVYKGISPEGV--SYLENLD-----EMALQTKNLEK 345
Db 760 ILEIKDVIQOEVIIEVEKVKIRK--KVEKGIKENHTESKDKVIGOEIITEVEKEIEK 816
Qy 346 NATDNISKLEFPAPSEKSHETDSTKEEAAKMEKEYSIKDSTKDDNSNPGKTDPEKGT 405
Db 817 QVEEGIK-----ENDTESKSKVIGOEIVIKG---DVNEEGENDKVTYKQEKVK- 861
Qy 406 EAYLEAIRKNIEMLKHKDKGNKEDYDLSK--NRDPINKQADAVVEKGLDKKEAEAIK 462
Db 862 EVKKEVKKKKKKKKKKKRNKKNERKDNVIGKEIKEDVNEKDTANKDKETIQEKEKEEVK 920

RESULT 11
ID 096229 PRELIMINARY; PRT; 951 AA.
AC 096229;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
GN PFB0680W.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Gardner M.J., Tetteh H., Carnucci D.J., Cummings L.M., Aravind L.,
RA Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,
RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Perera M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Science 282:1126-1132(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=3D7;
RC MEDLINE=22255705; PubMed=9804551;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlson J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
RA Partea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carnucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrett B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL:AE001410; AAC71925.2;
KW Hypothetical protein.
SQ SEQUENCE 951 AA; 112486 MW; AC0D889358A84F4F CRC64;

Query Match 7.6%; Score 182; DB 5; Length 951;
Best Local Similarity 21.8%; Pred. No. 0.23;
Matches 103; Conservative 78; Mismatches 181; Indels 110; Gaps 17;
Qy 25 GSDKSLNRELISAERPLNEQIAEAEDKIKKTYPPENKPGQSNYSFVDMNLRLAITRK 84
Db 161 GKQDISNSNAE--NRKDVKEGVKLEKKEIKISDHHVEENKKS-----DD 206
Qy 85 EKIEKERQSISSPLDNKLN-----VEDVSTNRKLLIDYDSTKSLDHRKFDPPDGLHQ 140

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```
Db 207 HKVEENKSDHKEVEKSKSDHKEVEKVEHEDEEDKKEKSEKNNKNNEND 266
QY 141 LDGPTLAEDIYIKIARIYEENDRAVFKIVKLNGLITESQAHTLEDEVAEVLQKI 200
Db 267 EDNDEISDEEDVDVEEDKNNENDIDDDK-----KETDTHLEEEENETIEKE 315
QY 201 IS-KEANVEEDENKPTSW-TENQAGRIPEKVT PMAIDGLAKGNDENVSTLTLTG 258
Db 316 FSKKKNKKNKDKOTKKEKSKDTEKESKDIEK-----EKSKDKE----- 353
QY 259 LEERTTYSEDNFRDFQYPPNFYALLKSIDSEKAKEETLITIMKTLIDFYKMYKGT 318
Db 354 -KEKSKDKEKEKDKKE-----KEKSKDIEKE-KEKDIDIEKSK-DTAKKEKDKD 403
QY 319 ISPEGVSYLENDEMAILOTKNKLEKNATDNISKLEPPASEKSH-----E 364
Db 404 IEKESK-----KDKELKNQNDKKEKDKDNEK-----KNDKODIHDNDENDMEETE 452
QY 365 EEDSTKEEAKKE-----KEYGSLKDKSTK-DDNSNPGKTDPEKGTAEVLEAI 412
Db 453 ENDEDEDEDEKNNKKNKKNKNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGN 512
QY 413 KNIEMLKHKHKKGNKEDYDLSKMDP-----INKQADAYVEKGIID 454
Db 513 NENNGENENENENENENENENENENENENENENENENENENENENENENENEN 564
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## RESULT 12

```
Q07380 PRELIMINARY; PRT: 1790 AA.
AC 007380; P89892;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical 206.5 kDa protein YD058W.
GN USOI OR YD058W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Bloescher H., Brandt P.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; 274106; CAA98621.1;
DR EMBL; 274105; CAA98620.1;
DR SGD; S0002216; USOI.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR006955; USOI_P115_C.
DR InterPro: IPR006953; USOI_P115_C.
DR Pfam; PF04871; USOI_P115_C.1.
DR Pfam; PF04869; USOI_P115_head.1.
SO SEQUENCE 1790 AA; 206450 MW; 90062544f55a52ee CRC64;
```

Query Match 7.5%; Score 181; DB 3; Length 1790;  
Best Local Similarity 19.9%; Pred. No. 0.34;  
Matches 118; Conservative 102; Mismatches 16; Indels 196; Gaps 28;

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QY 30 SLANRELTAERPLEQOIAEA--EEDKIKKTPPNKPGOSNYSVNDNLRLATTEKEKI 87
Db 748 SLOGETSTHENLEKILALNEHKEDEKQIIN--SSISLAKENFSIL----- 795
QY 88 EKEQOSIRSSPLDNKLAVEDVSTK---NRKLIDYSTKSGLDHKEFODD---PDGLHQ 140
Db 796 ETELKNVRS-LDMETQLRVLETCKENQTALEKYST---IHKQEDSIKLTLEKLET 850
QY 141 LDGPTLAEDIYIKIARIY-----EEN-----DRAVEKIVS 173
Db 851 ILSGKKAADGICINMGDLFALSREMAVEENCKNLQEKDKSVNHHQKSTSLKEDIAA 910
QY 174 KLNGLITES-----QAHTLEDEVAEVLQKLSKEANNVEEDPNKPTSWTENQAGKIP 227
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Db 911 KITTEIKAINENLEBKIOCNLSKEKEHISKELVEYKSRFQSHD-----NLVAKLT 961
QY 228 EKVTPMA-----AIODGLANGDENYNSLTTLNGLERTKTYSEDNFRDFO----- 275
Db 962 EKLKSLANNYKMOAENESLILKAVESKNNESSIQLSN-LQNKIDMSQEK-ENFQIEGNS 1019
QY 276 YFPNRYALLKSIDSEKAKEK-----EFLITIMKTLIDFYKMYKGTISPEGVSYL- 328
Db 1020 IEKNIELOKKTISDLEQTEELISKSDSKDEYESQISLKEKLETATANDENVNKISE 1079
QY 329 -----ENLDEMIA-----LQKNK-----LEKNAD----- 349
Db 1080 LKTEBELFAELAAKKNLKELETLETSEKALKVKNNEHLEEKIQLEKATERRQO 1139
QY 350 -----NISKLFPAPSEKSHEDTST-----KEAAKMEKEK-----GSLKD-----STKDONS 392
Db 1140 LNSLRANLESL-----EKEHEDLAQQLKYEEOJANKROQVNEELSQNDLITSTQONE 1194
QY 393 NPGGKTDPEKGTAEV-----LEAIKNIEMLKHKDKG----- 426
Db 1195 SIKKKNDELVEGVKAMKSTSEOSNLKKSSEIDALNLQIKELKKNETFEASLESIKSVE 1254
QY 427 -----NKEDYLSKMDPFIKQAD---AYVEKGIIDKEEAEAIK 462
Db 1255 SETYKIKELQDECNFKEKVESELEDKLASEDKNSKIUEL---QKSEKIK 1302
```

## RESULT 13

```
Q08145 PRELIMINARY; PRT: 3504 AA.
AC 08145;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
GN Pf14_0404.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-3D7;
RA MEDLINE=22255705; PubMed=1236864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.D., Suh B., Peterson J., Angiuoli S.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McPadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrrell B.,
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL; AE014822; AAN37017.1;
KW Hypothetical protein.
SO SEQUENCE 3504 AA; 408303 MW; B8454D48D55BE4F0 CRC64;
```

Query Match 7.5%; Score 180.5; DB 5; Length 3504;  
Best Local Similarity 20.5%; Pred. No. 1.3;  
Matches 104; Conservative 93; Mismatches 172; Indels 139; Gaps 22;

```
QY 32 HN-----RELTAE-----RLUNEQIAEA-----EDKIKKTPPNKPGQ----- 66
Db 982 HNLIQKNESYDETMNEYIISPSETINDEBNTPQYEEVSKNINNDKNGKRINNDOLE 1041
QY 67 ----SNYSFVDNLNLRLATTEKEKIKERQSISSPLDN-----KLNVEDVSTKKNRLID 118
Db 1042 SPLTSNEKRTDIDIH---IEEKIKDK---PIHNNDLQNEHKKHIIQD-----DKLE 1086
QY 119 DYVSTSGLDHKEFODDPLDGLHQDLPPLTAEDIYIKIARIYEENDRAVFKIVKLNGL 178
```



Db 1089 EXSTLPNSKEMK-----NISGDNINLNLNKKKEENHIIHENIEDTYSK 1134

Qy 179 GITESQAHLEDEVAEVLÖKLSKEANNYEEDPNKPTSWTEN-----QAGKI----- 226

Db 1135 DNEKNMÖNTIHHDDLG---KKDISRENTGEDISPNKYLNKNEYGLIDGKTKIYEENN 1191

Qy 227 PEKVEPMIAIODGLAENDEYV-----SNTLTJNLGLERKRTYSEDN 270

Db 1192 EEYVTDVSGENKNSGNSNDNIMPEYKKNKNSQENSEDNIMTEKNGKNSSEEMTDN 1251

Qy 271 FRDFOYFPNFYALKSIDSEKAEKETLITTKLIDPVKMKVYKGTISPEGVSYLEN 330

Db 1252 -----IMTEKNGKDSSEENANDNI-----MTEKNGKNSSQG-----N 1285

Qy 331 LDENIALQ---TKNKLEKATNIDISLFPAPSEKSHEDTST-----KEEAK----- 375

Db 1286 IDDNIMTEKNGKNSQENSEDDNIMTEYKKNKNSQENSEDDNIMTEKNGKNSSEEMTD 1345

Qy 376 --MEKEYGSLKDSKTDKNSNPGKTEDEPKGTAEYLAIRKNIEMLKHKDKKNGKEDYDL 433

Db 1346 NIMTEKNG--KDKSSEENANDNMT-EKNGKNSSEENADNIMTEKNGKNSSEENAD 1402

Qy 434 SKMRD--FLNKQADAYVEKGLDKEAE 459

Db 1403 NITRENGKNSQENSEDDNIMTEYXGE 1430

## RESULT 14

Q9SRD5 PRELIMINARY; PRT; 1871 AA.

AC 09SRD5:

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)

DE Putative heat shock protein, 53413-59028.

GN F28016.15.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,

RA Maiti R., Konnang C.M., Koo H., Fujii C.Y., Utterback T.R.,

RA Barnstead M.E., Bowman C.L., White O., Nielsen W.C., Fraser C.M.;

RT "Arabidopsis thaliana chromosome 1 BAC F28016 genomic sequence."

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC010718; AAP04452.1; -

DR InterPro: IPR002068; Hsp20.

DR PROSITE: PS01031; Hsp20; 1.

KW Heat shock.

SO SEQUENCE 1871 AA; 216899 MW; 52300C21F3DBF5A1 CRC64;

Query Match 7.5%; Score 180; DB 10; Length 1871;

Best Local Similarity 20.9%; Pred. No. 0.64;

Matches 117; Conservative 84; Mismatches 212; Indels 148; Gaps 22;

Qy 12 VIVLPFOAFPKP--GGSODKSLHNRLSAERPLNEQIAEAEDKIKKTPPEKPGQSNV 69

Db 1052 VIVEEETYPKDKHGTGGEHDHKEEOKENYAKAEKLTEDSFKVEIEHQ----- 1105

Qy 70 SEVDNLNLLRAITEKEIKEROSIRSSPLDNKLNVEDVSTKN--RKLIDDYDSTKSG 126

Db 1106 ---DHGELKRSMAQARQETEEKD-KTRAMEKNETYERRKQFDGSLKRLREGDEPGLG 1161

Qy 127 LDHKPDQDDGLHQLDGTPLT--AEDIVIKIARIYEENDRAVFD---KIYKLNGL 180

Db 1162 --HERGEDRIEELTEIISHKEKVKKKDEDYILRSODTGKVDLGERRRRSKÖRKIRH 1219

Qy 181 ITESQAHLEDEVAEVLÖKLSKEAN-----NVEEDPNKPTSWTENQAGKIPEKVTPT 232

Db 1220 SVEDEIGDQDEDEAEAAAVSHRNGSSRKQVOTIEESEK-----HKEONKIPETSNEP 1274

Qy 233 -----MAIIOGLAKGEN-----DETYSNTLTJNLGLERRTK 265

Db 1275 VNEDEBERVYKETEKEVAHVOLLEGTEKCKDDGBGRREKGGOMTAENNLRORFKT 1334

Qy 266 YSEDNFRDFOYFPNFYALKSID--SEKAEKETLITTKLIDPVKMKVYKGTI----- 319

Db 1335 KSPD-----GIYAKIOFTKEEEDDEKS-----QESSHYKVLVAEDGSLRNL 1378

Qy 320 ---SPEGVSYLENLDEMIALQTKNLEKNATD--NISKLFPAPSEKSHEDTST----- 369

Db 1379 EFSEKSTVSKMKLDESKKEBEHKIRKPTERSNAPYLEKQGNKNAEEMQDKIDR 1438

Qy 370 -KEEAKMEKEYSKLD-----EPKGTAEYLAIRKNIEMLKHKDKKNGKEDYDL--KMRDFIN 441

Db 1439 GKNOEIKGQEPYGLRNGEHDKITEYHGEKGTAEVSSSTKIQÖRKDELEKRPKSEIS 1498

Qy 400 -----EPKGTAEYLAIRKNIEMLKHKDKKNGKEDYDL--KMRDFIN 441

Db 1499 ENHINIEFDDSSODIEEKGSDQAEKYAKÖNKIOEVANDEK--KEETHISERVNEMA 1556

Qy 442 K--QADAYVEKGLDKEAE 459

Db 1557 KRILÖYESKANDDGSSKKNETE 1577

## RESULT 15

Q9LFE4 PRELIMINARY; PRT; 853 AA.

AC 09LFE4:

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)

DE Hypothetical 96.2 kDa protein.

GN F5E19.70.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,

RA Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,

RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RA Arabidopsis sequencing project;

RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL391147; CAC01837.1; -

DR InterPro: IPR002017; Spectrin.

DR SMART: SM00150; SPEC; 1.

KW Hypothetical protein.

SO SEQUENCE 853 AA; 96207 MW; EB7563A667F11AAD CRC64;

Query Match 7.5%; Score 179.5; DB 10; Length 853;

Best Local Similarity 20.3%; Pred. No. 0.27;

Matches 98; Conservative 82; Mismatches 209; Indels 93; Gaps 17;

Qy 38 AERPLNQLAEEADKIKKTPPENKPGQSNVFNVLNLLRAI-TEKEIKEROSIS 96

Db 30 AKRTVKN--SETSNNSPSTTPPHSR-----LSIDRSNPKSSSVERRSPKLP 76

Qy 97 SPLDNKLNVEDVSTKN-----RKLIDDYDSTKSGLDHKFQDDPDGLHQLDGTPLTAE 149

Db 77 PEKSGARAAAVGCTSPQTTTSLQIKEDLKANRISLSEKDKAKALDELKQAKKEAE 136

Qy 150 DIVHKIARIYEENDRAVPDKIVSKLNLGLITESQAHLEDEVAEVLÖKLS--KEANN 207

Db 137 QVTLKL-----DDAL-----KAÖKHVEENSEIKFQAVEAGIEAVON 173

Qy 208 YEEDPNKPTSWTENQAG--KIPEKVTPTMAIIOGLAK----- 242

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Db 174 NEELKKELETVKNOHSDSALVAVROELEKINEE---LAAAFDAKSKALSOAEDASKT 230
QY 243 ---GENDETVSNLTITLITNGL--ERRKTIYSEDNFRDFOYFPNFYALLKSIDSEKE 292
Db 231 AEIHAEKVDILSSSELTRLKALDSTREKTAISDNEMVAKLEDEIVVLKRDLESARGFEE 290
QY 293 AKKETLITIMKTLIDFVKMMVYGTISPPEGVSYLENLDEMIALOTKKNLEKNAT---D 349
Db 291 VKEKEMIVERKLANDLEAKKAESNAHSLSNEMOSKAKLEEQ--LEEANKLERSASVLE 348
QY 350 NISKLPPAPSEKSH-ETDST--KEEAAMEKEKYGSLKSTKDDNSNPGKTDPEPKTE 406
Db 349 SVMKOLEGSNDKLDHDETETITDLKERIVTLETTVAQKEDLEVSQRL-GSYEEYSKNE 407
QY 407 AYDEAIRKNINEMLKHKDKGNKEDYDLSKMRDFINKQADAYVEKGIIDKEEADAIKRIYS 466
Db 408 KEVEKIKSELETVEKKNRALKKEDDATSRVORLSEKSKLLSDLESSKEEKEKSKAME 467
QY 467 SL 468
Db 468 SL 469
```

Search completed: August 28, 2003, 10:23:19  
Job time : 72 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 28, 2003, 10:09:23 ; Search time 44 seconds  
(without alignments)  
1022.885 Million cell updates/sec

Title: US-09-554-945b-2  
Perfect score: 2402  
Sequence: 1 MGFLGTGWILVLVLPQAF.....EKGILDKEAEAIKRIYSSL 468

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1942	80.8	533	2 A37180	chromogranin/secre
2	191	8.0	2139	2 T18296	myosin heavy chain
3	183.5	7.6	2116	2 A26655	myosin heavy chain
4	182	7.6	665	2 B71609	hypothetical prote
5	181	7.5	1790	2 S67593	transport protein
6	181	7.5	2464	1 QRMSP1	microtubule-associ
7	180	7.5	1871	2 D96796	probable heat choc
8	179.5	7.5	853	2 T51505	hypothetical prote
9	174.5	7.3	1526	2 A45605	mature-parasite-in
10	173	7.2	1558	2 B71603	RESA-H3 antigen pr
11	172.5	7.2	1979	2 C71622	hypothetical prote
12	171	7.1	2269	2 T28677	rhostry protein -
13	170.5	7.1	2364	2 A56577	microtubule-associ
14	169.5	7.1	1134	2 A60234	IgA FC receptor pr
15	168.5	7.1	1164	1 FCSOAG	IgA FC receptor pr
16	169.5	7.1	1392	2 A43336	microtubule-vesicl
17	169.5	7.1	1427	2 S22695	restin - human
18	169	7.0	1005	2 A64465	hypothetical prote
19	169	7.0	1909	2 A45592	liver stage antige
20	169	7.0	3488	2 T34418	hypothetical prote
21	168	7.0	1252	2 B42771	reticulocyte-bindi
22	168	7.0	1272	2 C90593	hypothetical prote
23	165.5	6.9	746	2 T47237	myosin II heavy ch
24	165.5	6.9	1804	2 T34518	nestin - golden ha
25	165	6.9	2401	2 T28676	rhostry protein -
26	164.5	6.8	5327	2 T13564	microtubule-associ
27	163.5	6.8	719	2 A81358	hypothetical prote
28	163.5	6.8	926	2 T24923	hypothetical prote
29	163.5	6.8	1169	2 T18423	hypothetical prote

30	163	6.8	976	2 T01553	hypothetical prote
31	162	6.7	1192	2 A71623	probable secreted
32	162	6.7	2663	1 S28261	centromere protein
33	161.5	6.7	1127	2 T28317	ORF MSV156 hypothe
34	161.5	6.7	1164	2 T24806	hypothetical prote
35	161.5	6.7	1577	2 T19722	hypothetical prote
36	161.5	6.7	1875	2 S38173	myosin-like protei
37	161.5	6.7	2385	2 A32491	myosin heavy chain
38	161.5	6.7	2411	2 B32491	myosin heavy chain
39	161	6.7	944	2 S26710	spindle pole body
40	161	6.7	2510	2 T28160	hypothetical prote
41	160	6.7	1354	2 S74244	serine/threonine-s
42	159.5	6.6	1738	2 T14867	interactin - slime
43	159.5	6.6	2523	2 T18477	hypothetical prote
44	159	6.6	852	2 D72230	conserved hypothet
45	158.5	6.6	841	2 A86188	hypothetical prote

## ALIGNMENTS

### RESULT 1

A37180  
chromogranin/secretogranin-like vesicle protein precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-Feb-1992 #sequence\_revision 07-Feb-1992 #text\_change 30-Sep-1993  
C:Accession: A37180  
R:Ottinger, H.P.; Battenberg, E.F.; Tsou, A.P.; Bloom, F.E.; Sutcliffe, J.G.  
J. Neurosci. 10, 3135-3147, 1990  
A:Title: IB1075: a brain- and pituitary-specific mRNA that encodes a novel chromogranin  
A:Reference number: A37180; MUID:90376160; PMID:2204688  
A:Accession: A37180  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-533 <OTT>

Query Match 80.8%; Score 1942; DB 2; Length 533;  
Best Local Similarity 85.7%; Pred. No. 8e-89;  
Matches 379; Conservative 23; Mismatches 40; Indels 0; Gaps 0;

QY	16	PIQAFPPKGGSQDKSLHNRELSABRP	NEQIAEAEADKIKKTYPPENKPGQSNYSVDNL	75
DB	63	PNSFPKPEGGSQDKSLHNRELSABRP	NEQIAEAEADKIKKTYPSBKPSERNFSSVDNL	122
QY	76	NLLRAITEKEKIERQSI	RRSSPLDNKLNVEDVSTKNRKLDDYDSTKSGLDHKKFQDDP	135
DB	123	NLLRAITEKETVEKAKQSI	RRSSPFDNRLNVDADSTKNRKLDEYDSTKSGLDRKVQDDP	182
QY	136	DGLHOLDGTPUTAEIDVHKIAARI	YEENDRAVDFKIVSKLLNLGLLITESQAHTLEDEVAE	195
DB	183	DGLHOLDGTPUTAEIDVHKIATRI	YEENDRGVDFKIVSKLLNLGLLITESQAHTLEDEVAE	242
QY	196	VLOKLISKEANNYEEDPNKPTSWTEN	QAGKIEKVTPTMAAIOQLAKGENDETSTVNTLTL	255
DB	243	ALQKLISKEANNYEAEKPTSTRTEN	QDGKIEKVTPTVAATQDGTNRENDTSTVNTLTL	302
QY	256	TNGLERRTKTYSENDFRDFOYFPNF	YALLKSIDSEKAKEKETLIITIMKTLIDFVKMMYK	315
DB	303	SNGLERRTNPHRDDDFEELQYFPNF	YALLTSIDSEKAKEKETLIITIMKTLIDFVKMMYK	362
QY	316	YGTISPESGVSYLENDEMIALQTKN	LEKATDNISKLPAPSEKSHETDSTKEAAK	375
DB	363	YGTISPESGVSYLENDEMIALQTKN	LEKNTDTSKSLFPAPPEKSHETDSTKEAAK	422
QY	376	MEKEYGSLKDSKDDNSNPGGKTDEP	KGTAEYLAIRKNIWLKHKHKKNGKEDYLSK	435
DB	423	MEKEYGSLKDSKDDNSNLGKTDDEA	KGTAEYLAIRKNIWLKHKHKKNGKEDYLSK	482
QY	436	MRDFINKQADAYVEKGILDKKEE		457
DB	483	MRDFINQOADAYVEKGILIRKK		504



Science 282, 1126-1132, 1998  
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A:Reference number: A71600; MUID:99021743; PMID:9804551  
A:Accession: B71609  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-665 <GAR>  
A:Cross-references: GB:AE001410; GB:AE001362; NID:g3845245; PIDN:AAC71925.1; PID:g384524  
A:Experimental source: clone 3D7  
C:Genetics:  
A:Gene: PFB0680w

Query Match 7.6%; Score 182; DB 2; Length 665;  
Best Local Similarity 21.8%; Pred. No. 0.072;  
Matches 103; Conservative 78; Mismatches 181; Indels 110; Gaps 17;  
QY 25 SQDQSLNNRSLAERPLNEQIAEAEEDKIKKTYPPENKPGQSNYSFVDNLLRAITEK 84  
DB 160 GKQDISNSNAE--NKKDVKEGVKELEKKKEKISDDHKVFNKKK-----DD 205  
QY 85 EKIEKROSIRSSPLDNKLN---VEDVDSTKNRKLIDDYDSTKSGLDHKKFODDPGLHQ 140  
DB 206 HKVEENKSDHDKVEENKSDHKKIEEVKKVEEHEDEEDKKEKSNKNKDNKDN 265  
QY 141 LDGTPLTAEIDIVHKAARIYEENDRAVFDKIVSKLNLGLIPESQAHTLEDEVAEVLQKL 200  
DB 266 EDNDEISDEDEVDDEKNDIDDDK-----KETDKTHLEEEENELIEKE 314  
QY 201 IS-KEANYEEDPNKPTGW-TENQAGKIPEKVTMPAAODGLAKGENDETSTNTLTNG 258  
DB 315 FSDKKKNGKNDTKKSKDTEKSKDKIEK-----EKSKDKE----- 352  
QY 259 LERRTKTYSEDNFRDQVFPFPYALLKSDSEKAKEKETLITIMKTLIDFVKMVKYGT 318  
DB 353 -KEKSKDEKEKKDKE-----KEKSKDIEKE-KEKDKDIEKSK-DTAKEKEKDK 402  
QY 319 ISPEEGSVYLENDEMIALQTKNLEKNATDNISLFPAPSEKSH-----E 364  
DB 403 IEKEKS-----KDMELKNQNDKKDNEKK-----KNDKQDIHDDNDNDMEETE 451  
QY 365 ETDSTKEAAKME-----KEYSLKSDTK-DNSNPGGKTDEPKGTAYLRAI 412  
DB 452 ENDEDEDEDEENKKKKKKNGNENGSENGNENGNENKNESENE 511  
QY 413 KNIEWLKHKDKGNKEDYDLSKMRDF-----INKQADAYVEKGILD 454  
DB 512 NENENGNENENKENEKDKNKEIENVNANKENYKINKNSEIITKSNID 563

RESULT 5  
S67593  
transport protein USO1 - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein D252; protein YDLO58w  
C:Species: Saccharomyces cerevisiae  
C>Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text\_change 21-Jul-2000  
C:Accession: S67593; A38455; S30782  
R:Blöcker, H.; Brandt, P.  
submitted to the Protein Sequence Database, July 1996  
A:Reference number: S67587  
A:Accession: S67593  
A:Molecule type: DNA  
A:Residues: 1-1790 <BLQ>  
A:Cross-references: EMBL:Z74106; NID:g1431058; PID:e253003; PID:g1431059; MIPS:YDLO58w  
A:Experimental source: strain S288C  
R:Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonehara, T.; Yoda, K.; Yamasaki, M.  
J. Cell Biol. 113, 245-260, 1991  
A:Title: A cytoskeleton-related gene, USO1, is required for intracellular protein transp  
A:Reference number: A38455; MUID:91185402; PMID:2010462  
A:Accession: A38455  
A:Molecule type: DNA  
A:Residues: 1-389, 'TA', 392-724, 'S', 726-1790 <NAK>  
A:Cross-references: GB:X54378; NID:g4777; PIDN:CAA38253.1; PID:g4778  
A>Note: the authors translated the codon ACT for residue 768 as Ile

R:Hostetter, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E  
submitted to the EMBL Data Library, February 1993  
A:Description: An integrin analogue in Saccharomyces cerevisiae.  
A:Reference number: S30782  
A:Accession: S30782  
A:Molecule type: DNA  
A:Residues: 71-846, 'E', 848-923, 'K', 925-1252, 'I', 1254-1318, 'V', 1320-1460, 'S', 1462-1580  
A:Cross-references: EMBL:L03188  
C:Genetics:  
A:Gene: SGD:USO1; INT1  
A:Cross-references: SGD:S0002216; MIPS:YDLO58w  
A:Map position: 4L  
C:Keywords: coiled coil; transmembrane protein  
F:326-342/Domain: transmembrane #status predicted <TM1>  
F:394-410/Domain: transmembrane #status predicted <TM2>  
F:617-633/Domain: transmembrane #status predicted <TM3>

Query Match 7.5%; Score 181; DB 2; Length 1790;  
Best Local Similarity 19.9%; Pred. No. 0.28;  
Matches 118; Conservative 102; Mismatches 176; Indels 196; Gaps 28;  
QY 30 SLHNRELSAERPLNEQIAEA--EEDKIKKTYPPENKPGQSNYSFVDNLLRAITEKEKI 87  
DB 748 SLQTESPHENLTKEKIALTNEHKELDEKYQILN--SSHSLKENFSIL----- 795  
QY 88 EKEROSIRSSPLDNKLNVEDVDSTK---NRKLIDDYDSTKSGLDHKKFOD---PDGLHQ 140  
DB 796 ETELKNRDS-JDEMTQLDKRVLETCKENQTALEYKST-----IHQEDSITKLEKLET 850  
QY 141 LDGTPLTAEIDIVHKAARIY-----EEN-----DRAVFDKIVS 173  
DB 851 ILSQKKAEEDGINKMGKDLFALSREMQAEEVCKNQLQKBDKSNVNHQKETSLEKEDIAA 910  
QY 174 KLLNLGLIPES-----QAHTLEDEVAEVLQKLISKEANNYEDPNKPTSWTENQAGKIP 227  
DB 911 KITEIKAINENLEEMKIQCNLSKEKEHISKELVEYKSRFQSHD-----NLVAKLT 961  
QY 228 EKVTWMA-----ATQDGLAKGENDETSTNTLTNGLERRTKTYSEDNFRDFQ----- 275  
DB 962 EKLKSLANNYKDMAENSLIKAVESKNESLIQSN-LQNKIDSNSQEK-ENFQTERGS 1019  
QY 276 YPFPYALKSIDSEKAKEK-----ETLITIMKTLIDFVKMVKYGTISPESGVSYL-- 328  
DB 1020 IEKNIEQLKKTISDLTEQTKEEIISKSDSKDEYEQISLLKEKLETATTANDENVNKISE 1079  
QY 329 -----ENLDEMTA-----LOTNKK-----LEKNATD----- 349  
DB 1080 LPTKREELAEALAAAYKNLKNLETKLETSEKALKVEKNEHLEKKEKIQLEKATETKQ 1139  
QY 350 -----NISKLPAPSEKSHETDST---KEAAKMEKEY---GSLKD---STKDDNS 392  
DB 1140 LNSLRANLES-----EKEHEDLAQLKKYEQIANKERQYNEEISQLENDITSTQGENE 1194  
QY 393 NPGGKTDEPKGTAEY-----LEAIRKNIEWLKHKDKKGG----- 426  
DB 1195 SIKKKNDELEGEVKAAMKSTSEQSNLKKSEIDALNLQIKELKKNETNEASLESIKSVE 1254  
QY 427 -----NKEDYLSKMRDPIKQAD---AYVEKGILDKEEAFAIK 462  
DB 1255 SETVTKIKELQDECNFKEKEVSELEDKLSKEDKNKSKYLEL-----QKSEKIK 1302

RESULT 6  
QRMSP1  
microtubule-associated protein MAP1B - mouse  
N:Alternate names: microtubule-associated protein MAP1(X); microtubule-associated pro  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text\_change 01-Sep-2000  
C:Accession: S07549; S44387; A33645  
R:Noble, M.; Lewis, S.A.; Cowan, N.J.  
J. Cell Biol. 109, 3367-3376, 1989  
A:Title: The microtubule binding domain of microtubule-associated protein MAP1B conta  
A:Reference number: A33645; MUID:90094539; PMID:2480963

A:Accession: S07549  
A:Molecule type: mRNA  
A:Residues: 1-2464 <NO>  
A:CROSS-references: EMBL:X51396; NID:g52999; PIDN:CAA35761.1; PID:g53000  
R:Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.  
Arch. Biochem. Biophys. 310, 428-432, 1994  
A:Title: Binding of heat-shock protein 70 (hsp70) to tubulin.  
A:Reference number: S44387; MUID:94234720; PMID:8179328  
A:Accession: S44387  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 653-663, 'IC' <SAN>  
C:Superfamily: microtubule-associated protein MAP1B  
C:Keywords: microtubule binding; phosphoprotein; tandem repeat  
F:589-786/Domain: microtubule binding #status experimental <WTB>  
F:589-592, 639-642, 649-652, 655-658, 660-663, 668-671, 674-677, 679-682, 683-686, 687-690, 691-694  
R-K-E/D-X)  
F:1861-2064/Region: 17-residue repeats  
F:91, 116, 351, 888, 1124, 1153, 1168, 1208, 1662, 1877, 1918, 2003, 2030, 2054, 2083/Binding site: ph  
F:147, 969, 1336, 1562, 1563, 1702, 1708, 1990, 2057, 2063, 2419/Binding site: phosphate (Thr) (co  
F:1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 7.5%; Score 181; DB 1; Length 2464;  
Best Local Similarity 20.9%; Pred. No. 0.42;  
Matches 116; Conservative 85; Mismatches 188; Indels 166; Gaps 24;

QY 22 KPGSQDKSLNRLSARPLNEQIAEA-----EEDKIKKTYP--PENKPGQSNYSFVD 73  
DB 550 KPAVASKVRKESKEETPEVTKTSQVEKTPKVESKEKVLVKKDKPVKTESKP----- 600  
QY 74 NLNLLRAITEKEKEKERQSRSSPLDNKLVNEDVDSTKRNKLIDYDSTKSGLDHKKPD 133  
DB 601 -----SVTEKVSKEQSPKVAEVAEQATESPKVTKDKVVKKEIKTK--LEEKKEE 652  
QY 134 DP--DGLHQLDGTPL-----TAEDIVHKIAARIYEENDRAVDKIVSKLLNLGLITSQ 185  
DB 653 KPKKEVVKEDTKPLKDKPRKEVKEIKKEIKKE--ERKELKKEVKK-----ETP 703  
QY 186 AHTLEDEVAEVLQKLSKEANNYEDPNK-----PTSWTNOAGKIPE---- 228  
DB 704 LKDAKKEVKEKKEKKE-----EAPKEIKKISKQIKKSTPQSDTKKPSALKPKVAKK 759  
QY 229 ----KVTMAA--IOD-GLAK-----GENDETIVSNLT----- 253  
DB 760 EESTKKEPLAGKLKDKGVKVKKEGKTTEAAATAVGTAATTAATAVAAAGIAAGPVKE 819  
QY 254 -----TLNGLERTKTYSEDNFRDFQFPNFIYALLKSIDSEKAKE-----KET 298  
DB 820 LEAERSLMSPPDLTKDFELKAEEDIVAKDIPQLELIEDEKLKETQPGEAYVIQKET 879  
QY 299 LITIMKTLIDFVKVMVYGTISPFGVSVYLENDLMIALQTKNKL---EKNATDNISKL- 354  
DB 880 EVS-----KSAESPDDGITTTEGE--CEQTPPEEPVEKQGVDDIEKPE 924  
QY 355 -----FPAPSEKSHETSTKEAARKEKEYGLSKDSTKDDNSNPGGKTDEPKGTEAYL 409  
DB 925 DEGAGFEESSETGVDYEAKEATEAEPEED-CEDNAGSASAKSHSPTEDDSAKAEADVHL 983  
QY 410 EAIRNI-----EWLKK-----HDKKGNKEDY-----DLSKMRDFIN 441  
DB 984 KEKRESVSGDDRAEDMDVLEKGEAEQSEEEGEEEDKAEDAREEGYEPDKTEADYVN 1043  
QY 442 KOADAVVEKGILDK 456  
DB 1044 AVADKAAEAGVTEEQ 1058

RESULT 7

D96796  
probable heat shock protein, 53413-59028 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: D96796

RESULT 8

T51505  
hypothetical protein F5E19\_70 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C:Accession: T51505  
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.;  
submitted to the Protein Sequence Database, August 2000

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malli, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: D96796  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1871 <SPO>  
A:CROSS-references: GB:AE005173; NID:g6143906; PIDN:AAF04452.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F28016.15  
A:Map position: 1

Query Match 7.5%; Score 180; DB 2; Length 1871;  
Best Local Similarity 20.9%; Pred. No. 0.33;  
Matches 117; Conservative 84; Mismatches 212; Indels 148; Gaps 22;

QY 12 VLVLPIQAPP--GGSQDKSLNRLSARPLNEQIAEAEDKIKKTYPPENKPGQSNY 69  
DB 1052 VLVEEETYPKDKHTGGEDHNDHKEEQENVIKAEALNEDSPFKVEIEKQ----- 1105  
QY 70 SFVDNLNLLRAITEKEKEKERQSRSSPLDNKLVNEDVDSTKN---RKLIDDYDSTKSG 126  
DB 1106 ---DHGLKRSVMQAKRQETEEK--KTRAMEKNETVERKQTKDGLSLGREGDEPLOG 1161  
QY 127 LDHKPDQDQGLHQLDGTPLT--AEDIVHKIAARIYEENDRAVD---KIVSKLLNLGL 180  
DB 1162 --HERGEEDRIEELVETIEISDHKEVKKKDEYILRSQDTGKVDLGERERRSKQKRIHK 1219  
QY 181 ITESQHTLEDEVAEVLQKLSKEAN-----NYEEDPNKPTSWTENAGKIPEKVT- 232  
DB 1220 SVEDEIGDQDEDEAEAAAVSVNRNENGSSRRKVTQTIIEESEK-----HKQNKLPETSNPE 1274  
QY 233 -----MAAQDGLAKGN-----DETIVSNLTLTNGLERTKT 265  
DB 1275 VNEDEERVVEKETEVEAHVQVELEKTEKDDGEGREERKGGKGMATNLRQREKT 1334  
QY 266 YSEDNFRDFQFPNFIYALLKSID--SEKAKKKEKTLITIMKTLIDFVKVMVYGTI---- 319  
DB 1335 KSDD-----GIVRKIQETKEEPDEKKS---QESSSHVVKLVKVAEDGSLRNL 1378  
QY 320 ---SPEEGVSVYLENDLMIALQTKNKLKNATD--NISKLFAPAPSEKSHETDST---- 369  
DB 1379 EFSEKESVTYKMLKLDSEKKEBEHKIRKPTERSNAPVIEKQGNKNAEEEMQDKIDRR 1438  
QY 370 -KEEAKEKKEYGSLKD-----STKDDNSNPGGKT-- 399  
DB 1439 GKNQELKGQEPGVGLNGEHDKITEYHGEKGTAEVNSSTKIQQTKDELEKPRKPS 1498  
QY 400 -----EPKGTAEYLAIRKNIEWLKHKHDKGNKEDYDLS--KMRDFIN 441  
DB 1499 ENHNITHEFMDSSQSDIEKSGDQAEKAKQNKIQEVMNDEK--KEEYHISERSVRNEMA 1556  
QY 442 K---QADAVVEKGILDK 459  
DB 1557 KRILQVESKANDGSSKKKNETE 1577



Query Match 7.2%; Score 173; DB 2; Length 1558;  
Best Local Similarity 22.0%; Pred. No. 0.58;  
Matches 120; Conservative 91; Mismatches 204; Indels 130; Gaps 26;

QY 27 QDKSLHRELAE--RLNEQIAAEEDKIKKTPPENKPGQSN-----YSFVDNL-- 75  
DB 725 EENAVESNENVAENLEKLNRTVFNVLQKVEETVEISGESLENNEMDKAFSEIFDNYKG 784  
QY 76 ---NLLR-----AITEKEKIERQSRSSPLDNKLN-----VEDVDSTK-- 112  
DB 785 IQENLLTGMPRSIETSIIVQSEKVDL--NENVSSILDNIENRMKREGLNKLNISSTEGV 843  
QY 113 -----NRKLDDYD-----STKSGLDHKFQDDPGLHOLDGTPLTAEDI- 151  
DB 844 QETVTHEVQNVYVDVDPAMKQDFGLTINAEAGLKEMFNLED--VFKSESDDVITVEIK 902  
QY 152 -----VHKIAARIYEENDRAVDKIVSKLLNLGLLITESAHLTDEVAEVLQKLI--- 201  
DB 903 DEVOKEVEKETVSIIEEMEENIVD-----VLEEEKEDLTDKMIDAVEESIEIS 951  
QY 202 --SKEANNYEDPNKPTSWT-----ENQAGKIPEKVTMAAIOQGLAKGE---NDETVSN 251  
DB 952 SDSKEETESIKKEKDYSLVVEEQDNDMDSEVKVLELKNWEEELMKDAVEIND----- 1006  
QY 252 TLTITNGLERKTKTYSE---DNFRDFQVFPNFYALLKS-----IDSEKEAKEK--ETLIT 301  
DB 1007 ---ITSKLIETQELNEVEADLIKDMEKLEKALSDESKSEIIDAOKDITLKVIEERHD 1063  
QY 302 IMKTLIDFVKNM--VKYCTISPEEGSVYLENDEMIALQTK--NKLEKNATDNISKLPAP 358  
DB 1064 ITTTLDEVELKDVDEDKI---EKVSDLKDEEDILKEVKEIKESILEIDYELKTKTIE 1120  
QY 359 SEKSHEETDSTKEBAARKEYSGLKDKDSTKDDNSNPGGKTDEPKGKTEAYLEARKNTEW 418  
DB 1121 TDILEEKKEIKOHFEFEAEAEIKDLEADILAEVSSLEVEEKKLEEVHE--LKEEVEH 1179  
QY 419 LKHDK--KGNKEDYLSKMRDFNKQADAY---VEKGILDK-----EEAEAIK 462  
DB 1180 IISGDARIKGLEED--DLEEVDDLKGSITLMLKGMELGDMKESLEDVTAKLGERVESLK 1238  
QY 463 RIYSS 467  
DB 1239 DVLSS 1243

RESULT 11  
C71622  
hypothetical protein PFB0145C - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 21-Jul-2000  
C:Accession: C71622  
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;  
Perle, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.  
Science 282, 1126-1132, 1998  
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A:Reference number: A71600; MUID:99021743; PMID:9804551  
A:Accession: C71622  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1979 <GAR>  
A:Cross-references: GB:AE001375; GB:AE001362; NID:g3845105; PIDN:AACT71819.1; PID:g384510  
A:Experimental source: clone 307  
C:Genetics:  
A:Gene: PFB0145C

Query Match 7.2%; Score 172.5; DB 2; Length 1979;  
Best Local Similarity 21.7%; Pred. No. 0.83;  
Matches 107; Conservative 90; Mismatches 212; Indels 83; Gaps 20;

QY 30 SLHNRSLASRPLNEQIAEAE--DKTKKTPPENKPGQSNYSFV-----DNLNLR 79  
DB 143 SLSNKIVNYESKIEELEKELKVKDKNDNDNYENKLEKE--DFVKOKIDMLNEKENLLQ 201

QY 80 A-----ITEKEK--IEKERSIRSSPLDNKLNVEDVDSTKNRKLID-----DYDSTKSGLDH 129  
DB 202 EKELDINKREKKINEKKNLKEETFNHIEKYLEKKNKRETIISIEIIDIKKHLEKLI 261  
QY 130 KQDDPDGLHOLDGTPLTAEDIVHKTAARIYEEND--RAVFDKIVSKLLNLGLLITESQAH 187  
DB 262 EIKEKEDLENLKNLKSLENVLKELKGCYKKEKNETINSLNDNIEK-----EKYK 313  
QY 188 TLEDEVAEVLQK--LISKEANNYEEDPNKPTSWTENQAGKIPEKVTMAAIOQGLAKGEN 245  
DB 314 LLEYLEENKQIDLLNKQEKKEKERE--KEREKEKEKE-----YDTLKEK 364  
QY 246 DETVS-----NTLTNGLERKTKTY--SEDNFRDFQ--YFPN-----FYALLKSIDS 289  
DB 365 DEKISILEKVVHSIKVREMDIEKREHNFHMEDQLKDKNSFVKNQKLVYKCEIKNLT 424  
QY 290 EKEAKE-----KETLITIMKTLIDFVKNMVYGTISPPEGVSYLENDEMIALQT 339  
DB 425 ELEKKEKELKDIENTSVKKEINKLINQNEKEQILAFNKNHKEEIHGLKEELKESVKI-- 482  
QY 340 KNKLE-----KNATDNISKLPAPSEKSHETDSTKEAAKMEKESGLSKDSTKDDNSNPG 395  
DB 483 -TKIETQELQEWVDIKQKELDQLOEKYNAQIESISIELSKKEKYNQYKNYIEEINNLN 541  
QY 396 GKTDEP-----KGTEAYLEAIRKNIEMLKHKDKGNKEDYDLSKMRDFINKQADAY- 447  
DB 542 EKLEETNKETYNLQNNYTNEINNNDNIHMLNGNIKTMTQISTLKNVDHLLNEQIDKLN 601  
QY 448 VEKGILDKREEAE 459  
DB 602 NEKGTLSNKISE 613

RESULT 12  
T28677  
rhopty protein - Plasmodium yoelli  
C:Species: Plasmodium yoelli  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 01-Dec-2000  
C:Accession: T28677; C45521  
R:Keen, J.; Sinha, K.; Brown, K.; Holder, A.  
Mol. Biochem. Parasitol. 65, 171-177, 1994  
A:Title: A gene coding for a high molecular mass rhopty protein of Plasmodium yoelli  
A:Reference number: T20508; MUID:95021522; PMID:7935623  
A:Accession: T28677  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-2269 <KE>  
A:Cross-references: EMBL:L27838; NID:g457145; PID:g457146; PIDN:AAA21304.1  
R:Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.  
Mol. Biochem. Parasitol. 42, 241-246, 1990  
A:Title: Identification of the gene for a plasmodium yoelli rhopty protein. Multiple  
A:Reference number: A45521; MUID:91101660; PMID:2270106  
A:Accession: C45521  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 2131-2269 <KE2>  
A:Cross-references: GB:M34283

Query Match 7.1%; Score 171; DB 2; Length 2269;  
Best Local Similarity 20.9%; Pred. No. 1.2;  
Matches 112; Conservative 83; Mismatches 196; Indels 144; Gaps 22;

QY 13 LVLPIQAFPKPGSQDKSLHNRSLASRPLNEQIAEAEEDKIKKTPPENKPGQSNYSFV 72  
DB 7 LILPLMNQFGLNESMIKLNKSGILRKYTISNQI-----KNKLVNYSYPEGREG-----FT 57  
QY 73 DNLNL-----LRAITEKEK-----IEKERSIRSSPLDN-----KLN- 104  
DB 58 SSLELAKSWEKTKLETITELTNEETVLEKEIRELFKKYLDDEAEARKYLEGLKLELNK 117  
QY 105 -----VEDVDST-----KNRKLIDD-----YDSTKSGLDH 129  
DB 118 KIKDIIAEYKNTVELKKEIKENNAVIDELANOSPYKVTGYIENKNTIYNTIKSYFDO 177



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308 DFVKMVKYGTISPEGVSVYLENDIMIALQTNKL---EKNATDNLISKL-----FPAP 358
783 -----KGSASPDEGIITTEGE--CRQTPPELPVKGQGVDDTEKFEDEGAGFEES 833
359 SEKSHEETDTKTEAAKMEKEYSLKDKSTDDNSNPGKTDPEKPKTEA--YLEIAIRKNI 416
834 SEAGDYEEKAETEEAEPEDG--EDNVSGSASKHSPTDEETAKAEADVHIKKEKRESV 890
417 -----FWLKHDKKGNKEDYDLKMRDFINKQADAVYVEKGILDKPEAE 459
891 ASGDRAEDMDALEKGEAEQSEEEGEE-----DKAEDAREDEHPDKTEAE 940

RESULT 14
A60234
Iga Fc receptor precursor - Streptococcus agalactiae (strain SB35)
N:Alternate names: Iga-binding protein; protein Bac
N:Contains: beta antigen
C:Species: Streptococcus agalactiae
C:Date: 08-Dec-1992 #sequence.revision 08-Dec-1992 #text_change 26-Aug-1999
C:Accession: A60234; S14595; A60230
R:Heden, L.O.; Frithz, E.; Lindahl, G.
Eur. J. Immunol. 21, 1481-1490, 1991
A:Title: Molecular characterization of an Iga receptor from group B streptococci
with Iga-binding capacity.
A:Reference number: A60234; MUID:91257158; PMID:2044657
A:Accession: A60234
A:Molecule type: DNA
A:Residues: 1-1134 <HD>
A:Cross-references: EMBL:X58470; NID:946520; PIDN:CAAA1384.1; PID:946521
A:Note: the source is designated as group B streptococcus strain SB35
R:Heden, L.; Frithz, E.; Lindahl, G.
submitted to the EMBL Data Library, March 1991

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A:Description: Molecular characterization of an Iga receptor from group B streptococci fragments.

A:Reference number: S14595

A:Accession: S14595

A:Molecule type: DNA

A:Residues: 1-1134 <HE2>

A:Cross-references: EMBL: X58470; NID: g46520; PIDN: CAA41384.1; PID: g46521

R:Note: the source is designated as Streptococcus agalactiae

R:Lindahl, G.; Akerstroem, B.; Vaerman, J.P.; Stenbergh, L.

Eur. J. Immunol. 20, 2241-2247, 1990

A:Title: Characterization of an Iga receptor from group B streptococci: specific

```

A:Reference number: A60230; MOLD:91055597; PMID:2242758
A:Accession: A60230
A:Molecule type: protein
A:Residues: 'X',39-48,'X',50-52,'X',54-56 <LIN>
C:Superfamily: Iga Fc receptor
C:Keywords: cell wall; immunoglobulin receptor; tandem repeat; transmembrane protein
F:1-37/Domain: signal sequence #status predicted <Sig>
F:38-1134/Product: Iga Fc receptor #status experimental <MAT>
F:199-438/Domain: Iga binding #status predicted <IGAL>
F:439-826/Domain: Iga binding #status predicted <IGA2>
F:827-915/Region: proline-rich repeats
F:916-1101/Domain: cell wall-spanning #status predicted <CWS>
F:1102-1129/Domain: transmembrane #status predicted <TM>

Query Match          7.1%  Score 169.5;  DB 2;  Length 1134;
Best Local Similarity 21.4%;  Pred. No. 0.58;
Matches 123;  Conservative 78;  Mismatches 189;  Indels 185;  Gaps 25;

Qy      36  LSAERPLNE-----QIAEAEEDTKTKYPPENKPGQSNYSFVDNLNLLRAIT-EKEK  86
Db      149  LELENQFNETNRLHLTHKQHEVEKDKKAK----QQKTLKQSDTKVDLSNDKELNHQSK  204

Qy      87  IEK--ERQSTRSSPLDNKL-----NVEDVDSTKNRKLDDYDSTKSGLDHK  130
Db      205  VERMAEQKGTINEDKDSMLKIEIDIRKQAQAQAKKEDAEVKEEGLKLFSSSTKAGLDQE  264

Qy      131  FQDDPGDLGLDGTPLTAEDIVHKI-----AARTIEENDRAVFDKIYSKLLNLG  179

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	Query Match	7.1%	Score 169.5;	DB 2;	Length 1134;
	Best Local Similarity	21.4%;	Pred. No. 0.58;		
	Matches	123;	Conservative	78;	Mismatches 189; Indels 185; Gaps 25;
Qy	36	LSAERPLNE-----QIAEAEEDTKTKYPPENKPGQSINYSFVDNLLRLRAIT-EKEK	86		
Dd	149	LELENQFNETNRLRHITKHQEEVEKKRAK---CQKTLKOSDTPKRVLDNSIDKELNHOKSQ	204		
Qy	87	IEK--EQQRSTSSPLDNKL-----NVEDVDSCTKNRKLDDYDSTKSGLDHK	130		
Dd	205	VERMAEQKGITNEDKDSMLKKIEDI RQAQAQADKKDAEVKVREELGKLFESSYKAGLQDE	264		
Qy	131	FQDDPDGLHQDGTPLTAEDIVHKI-----AARIYEENDRAVFDKVIYSKLLNLG	179		
Dd	265	IOE-----HYVKKET--SSSEENTOKVDHEYANSILONLAOKSILEELDATTNTEOATOVKNOF	317		

QY 180 L-----ITPSQAHTLEDEVAEV-----LOKLISKE-----ANNYEE 210  
Db 318 LENAQKLKEIQPLIKETNVKLYKAMESLEQVEKELKHNSANLEDLVAKSKEIVREYEG 377  
QY 211 DPNKPTSWTE-----NOAGKIPEKVTMPAAIQDGLAGKENDETVSN 251  
Db 378 KLNQSKNLPKQLPEEAHSLKQVVEDFRKKFTSEQVTPKRVKRDLAANNQ---Q 434  
QY 252 TLTLNGLERTKTYSEDNFRDFOYFPNFYALLKSIDSEKAKEKETLITIMKTLIDFPVK 311  
Db 435 KIELTVSPENITVYEGED-----VKFTVTAKS-DS-----KTTLDPSD 471  
QY 312 MMVKG-TISPVEGVSYLENLD-----EMIALQTK-----NKLEKNATD 349  
Db 472 LLTKYNPSVSDRISTNYKTNTDNHKAIEITIKNLKLNESQVTLKAKDDSGNVVEKFTTI 531  
QY 350 NISKLFPAPSEKSHETDSTKEEAA-----KMEKEYGSLKD 385  
Db 532 TVQKKEEKQVPTPEQKDSKTEEVQPEKPSNDKNQLOELIKSAQOELEKLEKAIKELME 591  
QY 386 STKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKK---HDKKGNKEDYDLSKMRDFIN 441  
Db 592 Q-PEIPSNP---EYGIQKSIWESQKEPTQEAITSFKKIIGDSSSKYYTEHYFNKYKSDFMN 648  
QY 442 KQADAYVEKGILDKEEAE-----AIKRIYSS 467  
Db 649 YQLHAQME--MLTRKVVQVMKNKYPDNAEIKKIFES 681

RESULT 15  
FCSOAG  
Iga Fc receptor precursor - Streptococcus agalactiae  
N:Alternate names: beta antigen  
C:Species: Streptococcus agalactiae  
C:Date: 30-Jun-1992 #sequence.Revision 30-Jun-1992 #text\_change 16-Jul-1999  
C:Accession: S15330; S20240; S17038  
R:Jernstroem, P.G.; Chhatwal, G.S.; Timmis, K.N.  
Mol. Microbiol. 5, 843-849, 1991  
A:Title: The Iga-binding beta antigen of the c protein complex of Group B streptococci:  
A:Reference number: S15330; MUID:91312121; PMID:1857207  
A:Accession: S15330  
A:Molecule type: DNA  
A:Residues: 1-1164 <JER1>  
A:Cross-references: EMBL:X59771  
A:Accession: S20240  
A:Molecule type: protein  
A:Residues: 38-48 <JE2>  
R:Jernstroem, P.G.  
Submitted to the EMBL Data Library, August 1991  
A:Reference number: S17038  
A:Accession: S17038  
A:Molecule type: DNA  
A:Residues: 1-914, 'E', 916-1164 <JE3>  
A:Cross-references: EMBL:X59771; NID:946522; PIDN:CAA42442.1; PID:946523  
C:Superfamily: Iga Fc receptor  
C:Keywords: cell wall; immunoglobulin receptor; tandem repeat; transmembrane protein  
F:1-37/Domain: signal sequence #status predicted <SIG>  
F:38-1164/Product: Iga Fc receptor #status experimental <MAT>  
F:199-438/Domain: Iga binding #status predicted <IGAL>  
F:439-826/Domain: Iga binding #status predicted <IGAL2>  
F:827-945/Region: proline-rich repeats  
F:946-1131/Domain: cell wall-spanning #status predicted <CWS>  
F:1132-1159/Domain: transmembrane #status predicted <TMM>

Query Match 7.1%; Score 169.5; DB 1; Length 1164;  
Best Local Similarity 21.4%; Pred. No. 0.6;  
Matches 123; Conservative 78; Mismatches 189; Indels 185; Gaps 25;  
QY 36 LSAERPLNE-----QIAAEEDIKKTYPPENKPGOSNYSFVNLNLLRAIT-EKEK 86  
Db 149 LELENQFNETNRLHLHKQHEEVEKDKAK-----QOKTLKQSDTKVDLSNIDKELNHQKSO 204

QY 87 IEK--EROSIRSSPLDNKL-----NVEDVDSTKNRKLIDDYDSTKSGLDHK 130  
Db 205 VEKMAEQGITNEBKDSMLKKIEDIRKQAAQADKEDAEVKVREELGKLFSTKAGLDQE 264  
QY 131 FQDDPDGLHQLDGTPLTAEDIVHKI-----AARIYEENDRAVDFKIVSKLLNLG 179  
Db 265 IQE-----HVKKET--SSEENTQKDEHYANSLQNAQKSLLEELDKATTNQATQVKNQF 317  
QY 180 L-----ITPSQAHTLEDEVAEV-----LOKLISKE-----ANNYEE 210  
Db 318 LENAQKLKEIQPLIKETNVKLYKAMESLEQVEKELKHNSANLEDLVAKSKEIVREYEG 377  
QY 211 DPNKPTSWTE-----NOAGKIPEKVTMPAAIQDGLAGKENDETVSN 251  
Db 378 KLNQSKNLPKQLPEEAHSLKQVVEDFRKKFTSEQVTPKRVKRDLAANNQ---Q 434  
QY 252 TLTLNGLERTKTYSEDNFRDFOYFPNFYALLKSIDSEKAKEKETLITIMKTLIDFPVK 311  
Db 435 KIELTVSPENITVYEGED-----VKFTVTAKS-DS-----KTTLDPSD 471  
QY 312 MMVKG-TISPVEGVSYLENLD-----EMIALQTK-----NKLEKNATD 349  
Db 472 LLTKYNPSVSDRISTNYKTNTDNHKAIEITIKNLKLNESQVTLKAKDDSGNVVEKFTTI 531  
QY 350 NISKLFPAPSEKSHETDSTKEEAA-----KMEKEYGSLKD 385  
Db 532 TVQKKEEKQVPTPEQKDSKTEEVQPEKPSNDKNQLOELIKSAQOELEKLEKAIKELME 591  
QY 386 STKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKK---HDKKGNKEDYDLSKMRDFIN 441  
Db 592 Q-PEIPSNP---EYGIQKSIWESQKEPTQEAITSFKKIIGDSSSKYYTEHYFNKYKSDFMN 648  
QY 442 KQADAYVEKGILDKEEAE-----AIKRIYSS 467  
Db 649 YQLHAQME--MLTRKVVQVMKNKYPDNAEIKKIFES 681

Search completed: August 28, 2003, 10:24:17  
Job time : 47 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2003, 08:26:12 ; Search time 36 seconds  
(without alignments)  
611.347 Million cell updates/sec

Title: US-09-554-945b-2

Perfect score: 2402

Sequence: 1 MGFLGTGWTLLVLPLQIAF.....EKGILDKKEAEAKRIYSSL 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	ID	Description
1	2380	99.1	468	1 SG3_HUMAN	Q8wxd2 homo sapien
2	2093.5	87.2	471	1 SG3_MOUSE	P47867 mus musculus
3	2081.5	86.7	471	1 SG3_RAT	P47868 rattus norv
4	183.5	7.6	2116	1 MYS2_DICDI	P08799 dictyosteli
5	181	7.5	882	1 RAS0_PYFU	P58301 pyrococcus
6	181	7.5	1790	1 US01_YEAST	P25386 saccharomyc
7	181	7.5	2464	1 MAPB_MOUSE	P14873 mus musculus
8	170.5	7.1	2459	1 MAPB_RAT	P15205 rattus norv
9	169.5	7.1	1164	1 BAG_STRAG	P27951 streptococc
10	169.5	7.1	1427	1 REST_HUMAN	P30622 homo sapien
11	169	7.0	1005	1 RAS0_METJA	Q58718 methanococc
12	168	7.0	1251	1 RBP2_PLAVB	Q00799 plasmodium
13	166	6.9	700	1 TRDN_CANFA	P82179 canis famill
14	162.5	6.8	957	1 KFSC_HUMAN	O60282 homo sapien
15	162	6.7	2863	1 CENE_HUMAN	Q02224 homo sapien
16	162	6.7	5038	1 PCLO_MOUSE	Q9qvx7 mus musculus
17	161.5	6.7	1875	1 MLP1_YEAST	Q02455 saccharomyc
18	161	6.7	944	1 NUF1_YEAST	P32380 saccharomyc
19	159.5	6.6	2230	1 GOC4_HUMAN	Q13439 homo sapien
20	159	6.6	852	1 RAS0_THEMA	Q9X1X1 thermotoga
21	158.5	6.6	956	1 KFSC_MOUSE	P28738 mus musculus
22	157.5	6.6	1978	1 MYHB_CHICK	P10587 gallus gall
23	157	6.5	2022	1 ANP1_ONCVO	P21249 onchocerca
24	156.5	6.5	1969	1 MYSAL_CAEEL	P12844 caenorhabdi
25	156.5	6.5	1972	1 MYHB_HUMAN	P35749 homo sapien
26	156	6.5	839	1 COB2_YEAST	P53959 saccharomyc
27	156	6.5	1208	1 PCP1_SCHPO	Q92351 schizosacch
28	155.5	6.5	1526	1 MYS2_SCHPO	Q92516 schizosacch
29	155	6.5	705	1 TRDN_RABIT	Q28820 oryctolagus
30	154.5	6.4	997	1 SCPL_RAT	Q03410 rattus norv
31	154	6.4	727	1 MFPI_ARATH	Q91w85 arabidopsis
32	153.5	6.4	1130	1 YLI7_CAEEL	Q11102 caenorhabdi
33	153.5	6.4	2104	1 MYS3_SCHPO	Q14157 schizosacch

RESULT 1

ID	SG3_HUMAN	STANDARD;	PRT;	468 AA.
AC	Q8WXD2; Q96G83; Q96G88; Q9Y6G7;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Secretogranin III precursor (SgIII).			
GN	SCG3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Pituitary;			
RA	Song H., Peng Y., Huang Q., Dai M., Mao Y., Zhang Q., Mao M., Fu G.,			
RA	Luo M., Chen J., Hu R.;			
RT	"Human secretogranin III mRNA, complete cds.";			
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.			
RX	MEDLINE=22093564; PubMed=12098761;			
RA	Rong Y.P., Liu F., Zeng L.C., Ma W.J., Wei D.Z., Han Z.G.;			
RT	"Cloning and characterization of a novel human secretory protein: secretogranin III.";			
RL	Acta Biochim. Biophys. Sin. 34:411-417(2002).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain, and Lung;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahney J., Helton E., Kettelman M., Maman A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	-!- SUBCELLULAR LOCATION: Secreted. Neuroendocrine and endocrine secretory granules.			
CC	-!- TISSUE SPECIFICITY: Expressed in brain, heart, kidney, liver and skeletal muscle.			

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EMBL; AF078851; AAD44483.1; -  
DR EMBL; AF453583; AAL67431.1; -  
DR EMBL; BC014539; AAH14539.1; -  
DR EMBL; BC009511; AAH09511.1; ALT\_INIT.  
DR Genew; HGNC:13707; SCG3.  
KW Signal; Cleavage on pair of basic residues; Polymorphism.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 468 SECRETORANIN III.  
FT VARIANT 125 125 S -> N (in dSNP:2305710).  
FT CONFLICT 79 79 K -> R (IN REF. 1).  
FT CONFLICT 167 167 A -> V (IN REF. 1 AND 2).  
FT CONFLICT 272 274 EEL -> RDF (IN REF. 1).  
SQ SEQUENCE 468 AA; 52977 MW; 633AB7692A783808 CRC64;

Query Match 99.1%; Score 2380; DB 1; Length 468;  
Best Local Similarity 98.9%; Pred. No. 1.7e-107;  
Matches 463; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGFLGTGFWILVLPQAPKPGSQDSKLSHRELSEALPQLNQLAEAEEDKTKKTPP 60  
DB 1 MGFLGTGFWILVLPQAPKPGSQDSKLSHRELSEALPQLNQLAEAEEDKTKKTPP 60  
QY 61 ENKPGQSNYSFVDNLLRAITEKEKEKESQSRSSPLDNKLVNVEDVSTKKNKLDDY 120  
DB 61 ENKPGQSNYSFVDNLLRAITEKEKEKESQSRSSPLDNKLVNVEDVSTKKNKLDDY 120  
QY 121 DSTKSGLDHFKQDDPGLHQLDGTPLTAEDIVHKAIRIYEENDRAVFDKIVSKLLNGL 180  
DB 121 DSTKSGLDHFKQDDPGLHQLDGTPLTAEDIVHKAIRIYEENDRAVFDKIVSKLLNGL 180  
QY 181 ITESQAHTLEDEVAEVLQKLISKANNYEEDPNKPTSWTENQAGKIPEKVTMPAAIODGL 240  
DB 181 ITESQAHTLEDEVAEVLQKLISKANNYEEDPNKPTSWTENQAGKIPEKVTMPAAIODGL 240  
QY 241 AKGNETVSNLTTLTNGLERRTKYSSEDFRQYFPNFPYALLKSIDSEKEAKEKTLI 300  
DB 241 AKGNETVSNLTTLTNGLERRTKYSSEDFRQYFPNFPYALLKSIDSEKEAKEKTLI 300  
QY 301 TIMKTLIDFVKMVKYGTISPESGVSYLENDEMIALQTKNLEKNATDNISKLPAPSE 360  
DB 301 TIMKTLIDFVKMVKYGTISPESGVSYLENDEMIALQTKNLEKNATDNISKLPAPSE 360  
QY 361 KSHETDSTKEAAKKEKESGLKSDSTKDDNSNPGGKTDEPKGTEAYLEAIRKNIEWLK 420  
DB 361 KSHETDSTKEAAKKEKESGLKSDSTKDDNSNPGGKTDEPKGTEAYLEAIRKNIEWLK 420  
QY 421 KHKKGKEDYDLSKMRDFINQADAYVEKGIIDKEAEAEAIKRIYSSL 468  
DB 421 KHKKGKEDYDLSKMRDFINQADAYVEKGIIDKEAEAEAIKRIYSSL 468

RESULT 2  
SG3\_MOUSE  
ID SG3\_MOUSE STANDARD; PRT; 471 AA.  
AC P47867;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Secretorinan III precursor (SgIII).  
GN SCG3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

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EMBL; U02982; AAA56636.1; -  
DR MGD; MGI:103032; Scg3.  
KW Signal; Cleavage on pair of basic residues.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 471 SECRETORANIN III.  
SQ SEQUENCE 471 AA; 53326 MW; FCLE9C381AFC564 CRC64;

Query Match 87.2%; Score 2093.5; DB 1; Length 471;  
Best Local Similarity 87.9%; Pred. No. 9.1e-94;  
Matches 414; Conservative 17; Mismatches 37; Indels 3; Gaps 1;

QY 1 MGFLGTGFWILVLPQAPKPGSQDSKLSHRELSEALPQLNQLAEAEEDKTKKTPP 57  
DB 1 MGFLGTGFWILVLPQAPKPGSQDSKLSHRELSEALPQLNQLAEAEEDKTKKTPP 57  
QY 58 YPPENKPGQSNYSFVDNLLRAITEKEKEKESQSRSSPLDNKLVNVEDVSTKKNKLI 117  
DB 61 FPSEKPSSESNYSFVDNLLRAITEKEKEKESQSRSSPLDNKLVNVEDVSTKKNKLI 120  
QY 118 DDVSTKSGLDHFKQDDPGLHQLDGTPLTAEDIVHKAIRIYEENDRAVFDKIVSKLLN 177  
DB 121 DEYDSTKSGLDHFKQDDPGLHQLDGTPLTAEDIVHKAIRIYEENDRAVFDKIVSKLLN 180  
QY 178 LGLITESQAHTLEDEVAEVLQKLISKANNYEEDPNKPTSWTENQAGKIPEKVTMPAAIQ 237  
DB 181 LGLITESQAHTLEDEVAEVLQKLISKANNYEEDPNKPTSWTENQAGKIPEKVTMPAAIQ 240  
QY 238 DGLAKGNETVSNLTTLTNGLERRTKYSSEDFRQYFPNFPYALLKSIDSEKEAKEKE 297  
DB 241 DGFTRNDETVSNLTTLTNGLERRTNPHREDDFEELQYFPNFPYALLTSIDSEKEAKEKE 300  
QY 298 TLITIMKTLIDFVKMVKYGTISPESGVSYLENDEMIALQTKNLEKNATDNISKLPFA 357  
DB 301 TLITIMKTLIDFVKMVKYGTISPESGVSYLENDEMIALQTKNLEKNATDNISKLPFA 360  
QY 358 PSEKSHETDSTKEAAKKEKESGLKSDSTKDDNSNPGGKTDEPKGTEAYLEAIRKNIE 417  
DB 361 PSEKSHETDSTKEAAKKEKESGLKSDSTKDDNSNPGGKTDEPKGTEAYLEAIRKNIE 420  
QY 418 WLKHKHKGKEDYDLSKMRDFINQADAYVEKGIIDKEAEAEAIKRIYSSL 468  
DB 421 WLKHKHKGKEDYDLSKMRDFINQADAYVEKGIIDKEAEAEAIKRIYSSL 471

RESULT 3  
SG3\_RAT  
ID SG3\_RAT STANDARD; PRT; 471 AA.  
AC P47868;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Secretorinan III precursor (SgIII) (181075).  
GN SCG3.

OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95001263; PubMed=7917832;  
 RA Dopazo A., Lovenberg T.W., Danielson P.E., Ottiger H.-P.,  
 RA Sutcliffe J.G.;  
 RT "Primary structure of mouse secretogranin III and its absence from  
 RT deficient mice.";  
 RL J. Mol. Neurosci. 4:225-233(1993).  
 RN [2]  
 RP PRELIMINARY SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=90376160; PubMed=2204688;  
 RA Ottiger H.-P., Battenberg E.F., Tsou A.-P., Bloom F.E.,  
 RA Sutcliffe J.G.;  
 RT "1B1075: a brain- and pituitary-specific mRNA that encodes a novel  
 RT chromogranin / Secretogranin-like component of intracellular  
 RT vesicles.";  
 RL J. Neurosci. 10:3135-3147(1990).  
 CC -!- SUBCELLULAR LOCATION: Secreted. Neuroendocrine and endocrine  
 CC secretory granules.  
 CC -!- TISSUE SPECIFICITY: BRAIN- AND PITUITARY-SPECIFIC.  
 CC -----  
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 CC -----  
 DR EMBL: U02983; AAA56637.1; -;  
 KW Signal; Cleavage on pair of basic residues.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 471 SECRETOGRANIN III.  
 SQ SEQUENCE 471 AA; 53183 MW; 9777B3F885F33223 CRC64;  
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 Query Match 86.7%; Score 2081.5; DB 1; Length 471;  
 Best Local Similarity 87.0%; Pred. No. 3.4e-93;  
 Matches 410; Conservative 20; Mismatches 38; Indels 3; Gaps 1;  
 QY 1 MGFLGTGWILVLV---PIQAFKPGSQDKSLHNRELSAERPLNEQIAEAEDKIKKT 57  
 DB 1 MGFLWTGSMILVVLNSGPIQAFKPGSQDKSLHNRELSAERPLNEQIAEAEDKIKKT 60  
 QY 58 YPPENKPCQSNVFDVNLNLRATEKEKEKESQIRSSPLDNKLVNVEDVDSTKNRKL 117  
 DB 61 YPSEKSPSESNFSSVDNLLKKAITEKETVEKAKOSIRSSPFDNRLNVDDADSTKNRKL 120  
 QY 118 DDYDSTKSLGDKHKKFDDPDGLHOLDGTPLTAEIVHKTAARIYENDRAVDFKIVSKLLN 177  
 DB 121 DEYDSTKSLGDKKQDDPDGLHOLDGTPLTAEIVHKTAARIYENDRGVDFKIVSKLLN 180  
 QY 178 LGLITESQAHTLEDEVAELVLOKLSKEANNYEEDPNKPTSWTENQAGRIPEKVTPTMAAIQ 237  
 DB 181 LGLITESQAHTLEDEVAELVLOKLSKEANNYEAEKPTSTENQDGKIPEKVTPTVAATQ 240  
 QY 238 DGLAGKENDETVSNPLTNTGLNRTKTYTSEDNFRDQYFPNFYALLKSIDSEKAKEKE 297  
 DB 241 DGFNTRENDTVSNPLTNSGLNRTNPHRDDPFELQYFPNFYALLTSDSEKAKEKE 300  
 QY 298 TLITIMKTLIDFVKMWVYKGISPEGVSYLENLDEMIALQTKNKLKNAEDNISKLP 357  
 DB 301 TLITIMKTLIDFVKMWVYKGISPEGVSYLENLDETALQTKNKLKNTTDSKSLP 360  
 QY 358 PSEKSHETDSTKEAAKWEKYGSLKDKDSDNSPGSKTDEPKGTEAYLEARKNIE 417  
 DB 361 PPEKSHETDSTKEAAKWEKYGSLKDKDSDNSLGGKTDDEAKGKTEAYLEARKNIE 420  
 QY 418 WLKHKHDKGNKEDYDLSKMRDFINQADAYVEKGLDKEEAIAIKRIYSSL 468

DB 421 WLKHKHDKGNKEDYDLSKMRDFINQADAYVEKGLDKEEAIAIKRIYSSL 471  
 RESULT 4  
 MYS2\_DICDI  
 ID MYS2\_DICDI STANDARD; PRT; 2116 AA.  
 AC P08799;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Myosin II heavy chain, non muscle.  
 GN MHCA.  
 OS Dictyostelium discoideum (Slime mold).  
 CC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87092266; PubMed=3540939;  
 RA Warrick H.M., de Lozanne A., Levinwand L.A., Spudich J.A.;  
 RT "Conserved protein domains in a myosin heavy chain gene from  
 RT Dictyostelium discoideum.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:9433-9437(1986).  
 RN [2]  
 RP PHOSPHORYLATION SITES, AND MUTAGENESIS.  
 RC STRAIN=AX2;  
 RX MEDLINE=90353583; PubMed=2387408;  
 RA Lueck-Vielmeier D., Schleicher M., Grabatin B., Wippler J.,  
 RA Gerisch G.;  
 RT "Replacement of threonine residues by serine and alanine in a  
 RT phosphorylatable heavy chain fragment of Dictyostelium myosin II.";  
 RL FEBS Lett. 269:239-243(1990).  
 RN [3]  
 RP PHOSPHORYLATION SITES.  
 RX MEDLINE=88112226; PubMed=2828113;  
 RA Wagle G., Noegel A., Scheel J., Gerisch G.;  
 RT "Phosphorylation of threonine residues on cloned fragments of the  
 RT Dictyostelium myosin heavy chain.";  
 RL FEBS Lett. 227:71-75(1988).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 1-762.  
 RX MEDLINE=95345066; PubMed=7619795;  
 RA Fisher A.J., Smith C.A., Thoden J.B., Smith R., Holden H.M.,  
 RA Rayment I.;  
 RT "X-ray structures of the myosin motor domain of Dictyostelium  
 RT discoideum complexed with MgADP.Befx and MgADP.ALf4-.";  
 RL Biochemistry 34:8960-8972(1995).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1-762.  
 RX MEDLINE=95345067; PubMed=7619796;  
 RA Smith C.A., Rayment I.;  
 RT "X-ray structure of the magnesium(II)-pyrophosphate complex of the  
 RT truncated head of Dictyostelium discoideum myosin to 2.7-A  
 RT resolution.";  
 RL Biochemistry 34:8973-8981(1995).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.  
 RX MEDLINE=96206189; PubMed=8611530;  
 RA Smith C.A., Rayment I.;  
 RT "X-ray structure of the magnesium(II).ADP.vanadate complex of the  
 RT Dictyostelium discoideum myosin motor domain to 1.9-A resolution.";  
 RL Biochemistry 35:5404-5417(1996).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 1-762.  
 RX MEDLINE=97452580; PubMed=9305951;  
 RA Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.;  
 RT "X-ray structures of the MgADP, MgATPgammAS, and MgAMPNP complexes  
 RT of the Dictyostelium discoideum myosin motor domain.";  
 RL Biochemistry 36:11619-11628(1997).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.  
 RX MEDLINE=98070605; PubMed=9405148;  
 RA Bauer C.B., Kuhlman P.A., Bagshaw C.R., Rayment I.;

"X-ray crystal structure and solution fluorescence characterization of Mg<sub>2</sub>(3')-O-(N-methylanthraniloyl) nucleotides bound to the Dictyostelium discoidium myosin motor domain".  
J. Mol. Biol. 274:394-407(1997).

-1- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY ACTIN.

-1- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-1- SUBCELLULAR LOCATION: HIGHEST CONCENTRATION IN THE POSTERIOR CELL CORTEX.

-1- DOMAIN: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMN) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN BE FURTHER SPLIT INTO 2 GLOBULAR SUBFRAGMENTS (SI) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

-1- PTM: PHOSPHORYLATION INHIBITS THICK FILAMENT FORMATION AND REDUCES THE ACTIN-ACTIVATED ATPASE ACTIVITY.

-1- MISCELLANEOUS: DICTYOSTELIUM MYOSIN II HAS NO K(2)EDTA ATPASE ACTIVITY, PERHAPS CORRELATED WITH THE ABSENCE OF A CYS AT THE SH-1 POSITION (688).

-1- SIMILARITY: Contains 1 myosin-like globular head domain.

-1- SIMILARITY: Contains 1 IQ domain.

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EMBL; M14628; AAA33227.1; -  
PIR; A26655; A26655  
PDB; 1MMA; 03-DEC-97.  
PDB; 1MMD; 17-AUG-96.  
PDB; 1MMG; 03-DEC-97.  
PDB; 1MMN; 03-DEC-97.  
PDB; 1MND; 17-AUG-96.  
PDB; 1MNE; 17-AUG-96.  
PDB; 1VOM; 23-DEC-96.  
PDB; 1LVK; 28-JAN-98.  
PDB; 1DXX; 20-DEC-00.  
PDB; 1DQY; 20-DEC-00.  
PDB; 1DQZ; 20-DEC-00.  
PDB; 1DIA; 20-DEC-00.  
PDB; 1DIB; 20-DEC-00.  
PDB; 1D1C; 20-DEC-00.  
PDB; 1FWV; 20-DEC-00.  
PDB; 1FWW; 20-DEC-00.  
PDB; 1GBX; 17-JAN-01.  
PDB; 1JWY; 07-NOV-01.  
PDB; 1JX2; 07-NOV-01.  
DictyDb; DD01008; mhca.  
InterPro; IPR000048; IQ\_region.  
InterPro; IPR001609; myosin\_head.  
InterPro; IPR004009; Myosin\_N.  
Pfam; PF00612; IQ; 2.  
Pfam; PF00063; myosin\_head; 1.  
Pfam; PF02736; myosin\_N; 1.  
PRINTS; PR00193; MYOSINHEAVY.  
ProDom; PD000355; myosin\_head; 1.  
SMART; SM00015; IQ; 1.  
SMART; SM00242; MYSC; 1.  
PROSITE; PS50096; IQ; 1.  
Myosin; Coiled coil; Actin-binding; ATP-binding; 3D-structure;  
Calmodulin-binding; Methylation; Alkylation; Phosphorylation.  
DOMAIN 1 761 MYOSIN HEAD-LIKE.  
FT DOMAIN 762 791 IQ.  
FT DOMAIN 817 2116 COILED COIL (POTENTIAL).

QY 142 DGTPLTAEDIVHIAIRIYEENDRAVDKIVSKLLNLGLITESQAHTLEDEVAEVLQKLI 201  
Db 1135 GEEKKSLYDL-----KVKQESDMEALRNQISELQSTIAKLEKIKSTLEGEVARLOGELE 1188  
QY 202 SKE--ANNYEEDPNKPTSWENOGAKIPEKVT-----PMAIODGLAKGEN 245  
Db 1189 AEOLAKSNVEKQKKVLELDEKDSQALETAQAQALDKLKKLEQELSEVQTLSEANN 1248  
QY 246 D-----ETVSNITLTLANGLERRTKTYSEDNFRDQFPYPPNFYALKSIDS--EKE 292  
Db 1249 KVNDSSTNKHLETSPNLLKLEAEQAKQALEKKRLGLE-----SELKHVNEQLEEE 1302  
QY 293 AREKET-----LIIMTKTLDIFVKVMKYGTISPBEGVSYLE----- 329  
Db 1303 KKOKESENEKRVKVDLEKEVSELKDQIEEVASKAVTEAKNKKESELDEIKROYADVSSR 1362  
QY 330 --NLDSMIALQTKN-KLEKNATDNISKLPAPSEKSHETD-----STKEEAAMEKEY 380  
Db 1363 DKSVEQLTKLOAKNEELRWTAEEAQOLDRASERKKAFFDLEEAQVKNLEETAKKVKAE 1422  
QY 381 GSKLSTKDDNSPNPGKTDPEKGTKEAYLEAIRKNIEWLKHKDKGNKEDYDLKKRDFI 440  
Db 1423 KAMKKAETDYRSTKSELDAKNVSSQYVQIKRLNEE-----LSELSVL 1467  
QY 441 NKOADAYVPEKGLDKKEAEA 460  
Db 1468 --EADERCNSAIKAKKTAES 1486

RESULT 5

RA50\_PYRFU ID RA50\_PYRFU STANDARD; PRT; 882 AA.  
AC P58301;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE DNA double-strand break repair rad50 ATPase.  
GN RAD50 OR PF1167.  
OS Pyrococcus furiosus.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=2261;  
RN [1]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;  
RX MEDLINE=20485553; PubMed=11029422;  
RA Hopfner K.-P., Karcher A., Shin D., Fairley C., Tainer J.A.,  
RA Carney J.P.,  
RA "Mrell and Rad50 from Pyrococcus furiosus: cloning and biochemical  
RT characterization reveal an evolutionarily conserved multiprotein  
RL machine.";  
RL J. Bacteriol. 182:6036-6041(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;  
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;  
RT "The complete sequence of the Pyrococcus furiosus genome.";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 1-149.  
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;  
RX MEDLINE=20348838; PubMed=10892749;  
RA Hopfner K.-P., Karcher A., Shin D.S., Craig L., Arthur L.M.,  
RA Carney J.P., Tainer J.A.;  
RT "Structural biology of Rad50 ATPase: ATP-driven conformational  
RT control in DNA double-strand break repair and the ABC-ATPase  
RL superfamily.";  
RL Cell 101:789-800(2000).  
CC -I- FUNCTION: Involved in DNA double-strand break repair (DSBR). The  
CC rad50/mrell complex possesses single-strand endonuclease activity  
CC and ATP-dependent double-strand-specific exonuclease activity.  
CC Rad50 provides an ATP-dependent control of mrell by unwinding  
CC and/or repositioning DNA ends into the mrell active site.

CC -I- SUBUNIT: Forms a complex with mrell.  
CC -I- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL; AE010225; AAL81291.1; -  
DR PDB; 1F2T; 20-SEP-00.  
DR PDB; 1F2U; 02-AUG-00.  
DR PDB; 1I18; 30-MAY-01.  
DR PDB; 1L8D; 28-AUG-02.  
DR HAMAP; MF\_00449; -; 1.  
DR InterPro; IPR003439; ABC-transporter.  
DR InterPro; IPR003395; SMC\_N.  
DR Pfam; PF04423; Rad50\_zn\_hook; 1.  
DR Pfam; PF02463; SMC\_N; 1.  
DR ProDom; PD000006; ABC-transporter; 1.  
KW DNA repair; Hydrolase; ATP-binding; Coiled coil; 3D-structure;  
KW Complete proteome.  
FT NP\_BIND 30 37 ATP.  
FT DOMAIN 148 744 COILED COIL (POTENTIAL).  
SQ SEQUENCE 882 AA; 103839 MW; 3ADCBD250382A99E CRC64;  
  
Query Match 7.5%; Score 181; DB 1; Length 882;  
Best Local Similarity 21.0%; Pred. No. 0.082;  
Matches 119; Conservative 99; Mismatches 186; Indels 164; Gaps 23;  
  
QY 29 KSLNNR-----ELSAERPLNEQIAEAED-----KIKKTYPPENKPGOSNFSVD 73  
Db 178 KTNNRIKRYDRLARTENIEELIKENEQELQVLOEISKIEVLP-----SKRSKVD 230  
QY 74 NL--NLLRAITEKEKIEKERSIRSSPLDNKLNVEDVST-----KNRKL--IDD 119  
Db 231 MLRKEVLEETKVEIENSERLEKRRGDKRTLEERIKNTYEYLEKLEKEKELEQVKE 290  
QY 120 YDSTKSGLD-----HKFQDD-PDGLHQDGTPLTAEDIVHIAIRYE----- 161  
Db 291 ITSIKKVDVAYLALKEFKNEYLDKYKIEKELTRVEELINEIQRIEELNEKESEKEKLE 350  
QY 162 -----ENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAEVLQKLSKEANNY 208  
Db 351 NEKEILNKLAILEKHQHYEEIKAKKENLRQLKEKLGDSPEDIKKLLEETKK-TTI 409  
QY 209 EEDPNKPTSWENQAGKIPEKVTPTMAAIQDGL--AKGE-----NDETVSNTL----- 253  
Db 410 EERNEIT-----QRIGELKNKIGDLTAIEELKAKGKPCVCGRELTDREHRELLSKYHL 465  
QY 254 -----TLTNGLERRTKTYSE-----DNFRDQFPYPPNFYALKSID 288  
Db 466 DLNNSKNTLAKLDRKSELELRIDMETIKRTPLLTVAEQIRSEELNLYNLEK--- 522  
QY 289 SEKEAKEKETLITIMKTLDIFVKVMKYGTISPBEGVSYLENLEDEMA--LOTNKLEKN 346  
Db 523 IEKNATEYKLEELRTLEGRIRGLA-----EDLKLAPLEKKLALIHKKQLEKE 574  
QY 347 ATDNISKLPAPSEKSHETDSTKEAAKMEKEYSLKSDTKD-----DNSNPGGK 397  
Db 575 LKELNKL-ESFGFKSVEDLSKLELEIYKRYLTLLNSKKELEITQREIAKAKETLEM 633  
QY 398 TDEPKGKTAYLEAIRKNIEWLKHKDKGNKEDY-----DLSK 435  
Db 634 SPEELAEVEADIERIEKLSQLK---QKYNEEYKKRKEEKELEKARLEAQKKELEK 690  
QY 436 MRDFINKQADAYVEKGLDKKEAEAIKR 463  
Db 691 RRDITK-----STLEKLAKEENRERVKK 714

RESULT 6										
D	USOL_YEAST	STANDARD;	PRT;	1790	AA.					
C	P25386;									
WT	01-MAY-1992	(Rel. 22, Created)								
TT	01-MAY-1992	(Rel. 22, Last sequence update)								
DT	16-OCT-2001	(Rel. 40, Last annotation update)								
DE	Intracellular protein transport protein USOL.									
DE	USOL OR INT1 OR YDL058W.									
GN	Saccharomyces cerevisiae (Baker's yeast).									
OS	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;									
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.									
OX	NCBI_TaxID=4932;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RC	STRAIN=X2180-1A;									
RC	MEDLINE=91185402; PubMed=2010462;									
RA	Nakajima H., Hirata A., Ogawa Y., Yonehara T., Yoda K.,									
RA	Yamasaki M.;									
RT	"A cytoskeleton-related gene, usol, is required for intracellular									
RT	protein transport in Saccharomyces cerevisiae.";									
RL	J. Cell Biol. 113:245-260(1991).									
RL	[2]									
RN	SEQUENCE OF 782-1790 FROM N.A.									
RP	Hostetter M.K., Herman D.J., Bendel C.M., McClellan M., Tao N.,									
RA	Kendrick K.E.;									
RA	Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.									
RL	[3]									
RP	SEQUENCE OF 1-8 FROM N.A.									
RA	Bai Y., Symington L.S.;									
RA	Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.									
RL	-1- FUNCTION: REQUIRED FOR PROTEIN TRANSPORT FROM THE ER TO THE GOLGI									
CC	COMPLEX.									
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR									
CC	MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE									
CC	ER AND THE GOLGI COMPLEX.									
CC	-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED									
CC	OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL									
CC	COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.									
CC	-1- SIMILARITY: BELONGS TO THE VDP/USOL/YBL047C FAMILY.									
CC	-----									
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CC	the European Bioinformatics Institute. There are no restrictions on its									
CC	use by non-profit institutions as long as its content is in no way									
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>									
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).									
CC	-----									
DR	EMBL; X54378; CAA38253.1; -									
DR	EMBL; L03188; AAB00143.1; -									
DR	EMBL; U53668; AAB66659.1; -									
DR	SGD; S0002216; USOL.									
DR	InterPro; IPR002017; Spectrin.									
DR	InterPro; IPR006955; Usol_p115_c.									
DR	InterPro; IPR006953; Usol_p115_head.									
DR	Pfam; PF04871; Usol_p115_C; 1.									
DR	Pfam; PF04869; Usol_p115_head; 1.									
DR	Transport; Protein transport; Golgi stack; Cytoskeleton; Coiled coil.									
DR	DOMAIN	1	724	GLOBULAR HEAD.						
FT	DOMAIN	725	1790	COILED COIL (POTENTIAL).						
FT	DOMAIN	465	487	CHARGED (HYPER-HYDROPHILIC).						
FT	DOMAIN	991	1790	DISPENSABLE FOR THE PROTEIN FUNCTION.						
FT	DOMAIN	1172	1786	ASP/GLU-RICH (ACIDIC).						
FT	CONFLICT	847	847	G -> E (IN REF. 2).						
FT	CONFLICT	924	924	E -> K (IN REF. 2).						
FT	CONFLICT	1253	1253	V -> I (IN REF. 2).						
FT	CONFLICT	1319	1319	I -> V (IN REF. 2).						
FT	CONFLICT	1461	1461	N -> S (IN REF. 2).						
FT	CONFLICT	1581	1581	G -> S (IN REF. 2).						
FT	CONFLICT	1600	1600	I -> V (IN REF. 2).						
FT	CONFLICT	1661	1661	R -> S (IN REF. 2).						
FT	CONFLICT	1772	1772	D -> DEEDDEE (IN REF. 2).						

SQ	SEQUENCE	1790	AA:	206424	MW:	6CE2B216E9FD4818	CRC64:	
	Query Match	7.5%;	Score 181;	DB 1;	Length 1790;			
	Best Local Similarity	19.9%;	Pred. No. 0.19;					
	Matches 118;	Conservative 102;	Mismatches 176;	Indels 196;	Gaps 28;			
Qy	30	SLHRELASARPLNEQIAEA--BEDKIKKTYPPENKPGOSNYSFVNLNLLRAITEKEKI	87					
Db	748	SLOTETESTHENLTKLIALTNEHKLDEKYILN--SSHSLKLENFSIL-----	795					
Qy	88	EKERQSTRSPDLNKLNVEDVSTK---NPKLDDYDSTKSLGDLHFKFODD---PDGLHQ	140					
Db	796	ETELKNYRDS-LDEMTQLRDVLETKDKENQATLLEYKST----IHKQDSIKTLEKGLT	850					
Qy	141	LDGTPLTAEADIVHKIAARIY-----EEN-----	173					
Db	851	ILSOKKKAEDGINKMGKDLFALSREMOQAVEENCKNLQKEKDSNVNHNQKETSCLKEDIAA	910					
Qy	174	KLLNLGLITES-----QAHTLEDEVAEVLQKLISKEANNYEEDPNKPPTSWTENQAGKP	227					
Db	911	KITEIKAINENLEEMKIQCNNLKSEKHEHISKELVEYKSRFQSHD-----NLVAKLT	961					
Qy	228	EKVTPMA-----AIODGLAKGENDETQVNTLTLTNGLERRTKTYSEDNFRDFQ-----	275					
Db	962	EKLKSLANNYKMQAENESLIKAVEESKNESSTQLSN-LQNKIDSNQOEK-ENFOIERGS	1019					
Qy	276	YFPNFYALLKSIDSEKAKEK-----ETLITIKMTLIDFVMMVKYGTISPESGVSYL--	328					
Db	1020	IEKNIEQLKTTISDLEQTKELIISKSDSDEVESQISLLKEKLETATTANDENVNKISE	1079					
Qy	329	-----ENDEMIA-----LQTKNK-----LEKNATD-----	349					
Db	1080	LTKTREELEALAAAYKNLKNLETKLETSEKALKEVKEHNEHLEKEIKLEKATEYKQ	1139					
Qy	350	-----NISKLFAPAPSEKSHETDST-----KEEAARMEKEY-----GSLKD-----STKDDNS	392					
Db	1140	LNSLRANLSE-----EKEHEDLAAQLKYEEOJANKERQYNEISQLNDEITSTQONE	1194					
Qy	393	NPQKTDTPKQKTEAY-----LEATRKNIEMWLKKHDKKG-----	426					
Db	1195	SIKKKNDELEGEVAMKSTSEEQSNLKKKSEADALNLQTKELKKKNTNEASLESIKSVE	1254					
Qy	427	-----NKEDYDLKMRDFINKQAD---AYVEKILDKKEAEAIK	462					
Db	1255	SETVKIKELQDECNFKKEVSELEDKLASEDKNSKYLEL-----QKESEKIK	1302					
RESULT 7								
MAPB_MOUSE	STANDARD;	PRT;	2464	AA.				
ID	MAPB_MOUSE							
AC	P14873;							
DT	01-APR-1990	(Rel. 14, Created)						
DT	01-APR-1990	(Rel. 14, Last sequence update)						
DT	28-FEB-2003	(Rel. 41, Last annotation update)						
DE	Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))							
DE	[Contains: MAP1 light chain LC1].							
GN	MAP1B OR MTAPIB OR MTAP5.							
OS	Mus musculus (Mouse).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
OX	NCBI_TaxID=10090;							
RN	[1]							
RP	SEQUENCE FROM N.A., AND DOMAIN.							
RC	STRAIN=Swiss Webster; TISSUE=Brain;							
RX	MEDLINE=90094539; PubMed=2480963;							
RA	Noble M., Lewis S.A., Cowan N.J.;							
RT	"The microtubule binding domain of microtubule-associated protein							
RT	MAP1B contains a repeated sequence motif unrelated to that of MAP2							
RT	and tau.";							
RL	J. Cell Biol. 109:3367-3376(1989).							
CC	-1- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.							
CC	PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES							
CC	THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAP1B BINDS TO AT LEAST							

Q	SEQUENCE	1790	AA; 206424	MW; 6CE2B216E9FD4818	CRC64;		
	Query Match	7.5%;	Score 181;	DB 1;	Length 1790;		
	Best Local Similarity	19.9%;	Pred. No. 0.19;				
	Matches 118;	Conservative 102;	Mismatches 176;	Indels 196;	Gaps 28;		
yy	30	SLHNRELSAERPLNEQIAEA--EEDKIKKTYPPENKPGQSNYSFVDNINLLRAITEKEKI	87				
bb	748	SLQTESTHENLTETKLIATNEHKEDELKQYILN---SSHSLKENFSIL-----	795				
yy	88	EKERSQSRSSPLDNKLNVEDVSTK---NRKLIDDYDSTKGLDGHKFDD---PDGLHQ	140				
bb	796	ETELKNVRDS--LDEMTQLRDVLETKDENQATALLEYKST---IHQKDSIKTLEKGLT	850				
yy	141	LDGTPLTAEIDIVHKIAARIY-----EEN-----DRAVPDKIVS	173				
bb	851	ILSOKKKAEDGINKMGKDLFALSREMQAVECNKLNQKEKDSNNVHOKETSKLAKEDIAA	910				
yy	174	KLLNLGLITES-----QAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTNOAGKIP	227				
bb	911	KITEIKAINENLEEMKIQCNLNSKEKEHISKELVEYKSRFQSHD-----NLVAKLT	961				
yy	228	EKVTPMA-----AIODGLAKGENDETVSNLTITNGLERTKTYSEDNFRDFQ----	275				
bb	962	EKLKSLANNYKDMQAENESLIKAVEESKNESIQLSN-LQNKIDSMSQEK-ENFQIERGS	1019				
yy	276	YFPNEYALLKSIDSEKAEEK-----ETLITIMTKTLIDFVKKMVKYGTISPPEGVSYL--	328				
bb	1020	TEKNIEQLKTYISDLEQTKKEEIIISKSDSKDEYESQISLLKKEKLETATTANDENVNKISE	1079				
yy	329	-----ENDEMTA-----LQTKNK-----LEKNATD----	349				
bb	1080	LTKTRELEAEALAYKLNKLETKLETSEKALKEVKEENEHLKKEIQLEKATEETKQO	1139				
yy	350	-----NISKLPAPSEKSHETDST---KEEAARMEKEY-----GSLKD---STKDDNS	392				
bb	1140	LNSLRANLES-----EKEDHLAQLKYEQLANKERQYNEEISQLNDEITSTQOENE	1194				
yy	393	NPGGKTDEPKGTEAY-----LBAIRKNIEWLKHKHKKG-----	426				
bb	1195	SIKKKNDLEGEVGMKMTSEQSNLKKSEIDALNLQIKELKKNNETNASLLESTKSVE	1254				
yy	427	-----NKEDYLSKMRDFINKQAD---AYVEKGILDKKEAEAIK	462				
bb	1255	SETVVIKELQDCNFKKEVSELEDKKASEDKNSKYLEL-----QKSEKIK	1302				
RESULT 7							
MAPB_MOUSE							
ID	MAPB_MOUSE	STANDARD;	PRT;	2464	AA.		
AC	P14873;						
DT	01-APR-1990	(Rel. 14, Created)					
DT	01-APR-1990	(Rel. 14, Last sequence update)					
DT	28-FEB-2003	(Rel. 41, Last annotation update)					
DE	Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))						
DE	[Contains: MAP1 light chain LC1].						
GN	MAP1B OR MTAP1B OR MTAP5.						
OS	Mus musculus (Mouse).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
OX	NCBI_TaxID=10090;						
OX	[1]						
RN	SEQUENCE FROM N.A., AND DOMAIN.						
RP	STRAIN=Swiss Webster; TISSUE=Brain;						
RC	MEDLINE=90094539; PubMed=2480963;						
RX	Noble M., Lewis S.A., Cowan N.J.;						
RA	"The microtubule binding domain of microtubule-associated protein						
RT	MAP1B contains a repeated sequence motif unrelated to that of MAP2						
RT	and tau.";						
RL	J. Cell Biol. 109:3367-3376(1989).						
CC	-1- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.						
CC	PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES						
CC	THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAP1B BINDS TO AT LEAST						
CC							



CC TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS  
CC MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN  
CC STABILIZING MICROTUBULES.  
CC -!- SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE  
CC WITH MAP1A AND MAP1B PROTEINS.  
CC -!- DOMAIN: Has a highly basic region with many copies of the sequence  
CC KKEE and KKEI/V, repeated but not at fixed intervals, which is  
CC responsible for the binding of MAP1B to microtubules.  
CC -!- PTM: LC1 IS COEXPRESSED WITH MAP1B. IT IS A POLYPEPTIDE GENERATED  
CC FROM MAP1B BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH  
CC BOTH MAP1A AND MAP1B. IT INTERACTS WITH THE AMINO-TERMINAL REGION  
CC OF MAP1B.  
CC -!- SIMILARITY: TO MAP1A.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X51396; CAA35761.1;  
CC PIR; S07549; QRMSP1.  
CC MGD; MGI:1306778; Mtap1b.  
CC GO; GO:0016358; P:dendrite morphogenesis; IMP.  
CC GO; GO:0001578; P:microtubule bundling; IMP.  
CC InterPro; IPR000102; MAP1B\_neuraxin.  
CC Pfam; PF00414; MAP1B\_neuraxin; 10.  
CC PROSITE; PS00230; MAP1B\_NEURAXIN; 7.  
CC Microtubules; Repeat; Phosphorylation.  
CC CHAIN ? 2464 MAP1 LIGHT CHAIN LC1.  
CC REPEAT 1874 1890 MAP1B 1.  
CC REPEAT 1891 1907 MAP1B 2.  
CC REPEAT 1908 1924 MAP1B 3.  
CC REPEAT 1925 1941 MAP1B 4.  
CC REPEAT 1942 1958 MAP1B 5.  
CC REPEAT 1959 1975 MAP1B 6.  
CC REPEAT 1993 2009 MAP1B 7.  
CC REPEAT 2010 2026 MAP1B 8.  
CC REPEAT 2027 2043 MAP1B 9.  
CC REPEAT 2044 2060 MAP1B 10.  
CC DOMAIN 589 787 KKEE AND KKEI/V REPEATS).  
CC SEQUENCE 2464 AA; 270408 MW; FBD3DD99CFBDA87 CRC64;  
Query Match 7.5%; Score 181; DB 1; Length 2464;  
Best Local Similarity 20.9%; Pred. No. 0.28;  
Matches 116; Conservative 85; Mismatches 188; Indels 166; Gaps 24;  
QY 22 KPGSQDKSLHNRSLAERPLNEQIAEA-----EEDIKKITYP--PENKPGQSNYSFVD 73  
DB 550 KPVASKSVKRSKEETPEVTQTSQVEKTPKVESKEKVLVKDKPKVKTESKP----- 600  
QY 74 NLMLRAITEKEKIEKQSRSSPLDNKLVNEDVDSTKNRKLIDYDSTKSLGDKHFKQD 133  
DB 601 -----STKEVSKSEKQSPKVAEAKQATESPKYTKDKVKKEIKTK--LEEKEE 652  
QY 134 DP--DGLHQLDGTPL-----TAEDIVHKIARIYEENDRAVDFDKIVSKLLNLGITESQ 185  
DB 653 KPKKEVKKEDKTPKDKPKKEKVEKKEIKKE--ERKELKKEVKK-----ETP 703  
QY 186 AHTEDEVAEVLQKLISKEANNYEEDPNK-----PTSWTENQAKIPE---- 228  
DB 704 LKDAKKEVKKKEKKEKVEK-----EKEPKKEIKKIDKIKKSTPQSDTKPKSAKPKVAKK 759  
QY 229 ----KVTPMAA--IOD-GLAK-----GENDEIVSNLT----- 253  
DB 760 EESTKPELAGKLKDKGVKVKKEGKTTEAAATVAGTAATAVAAAGTAASGPVKE 819  
QY 254 -----TLNGLERRRTKTSYSEDNFRDFOYFPNFPYALLKSIDSEKEAKE-----RET 298  
DB 820 LEAERSLSSPPDLTKDFEELKAEIDVAKDVKPKQLEIEDEKLEKETQPGYVIQKET 879

QY 239 LITIMKTLIDFVKMVKYGTISPESGVSYLENLDEMIALQTKNKL---EKNATDNISKL- 354  
DB 880 EVS-----KGSASPDSGITTEGE-CEQTPPELEPVKEQGVDDIERFE 924  
QY 335 -----FPAPSEKSHETDSTKEAAKMEKEYGSLKSDKDDNSNPGGKTDEPKGKTEAYL 409  
DB 925 DEGAFFESSETGDYEKAETEAPEPED--GEDNAGSGSASKHSPTEDDESAKAEADVHL 983  
QY 410 EAIRKNI-----EWLKK-----HDKKGNKEDY-----DLSKMRDFIN 441  
DB 984 KEKRESVYSGDDRAEDMDVLEKGEAEQSEEEGEEKDAEDAREGEYDPKTEAEDYVM 1043  
QY 442 KQADAYVEKGILDKE 456  
DB 1044 AVADKAAEAGVTEEQ 1058  
RESULT 8  
MAPB\_RAT  
ID MAPB\_RAT STANDARD; PRT; 2459 AA.  
AC P15205; Q62958; Q9ER21; Q9QW92;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Microtubule-associated protein 1B (MAP 1B) (Neuraxin) [Contains: MAP1  
DE light chain LC1].  
GN MAP1B.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE OF 1-142 FROM N.A.  
RC STRAIN-Sprague-Dawley; TISSUE-Testis;  
RX MEDLINE=96257242; PubMed=8666295;  
RA Liu D., Fischer I.;  
RT "Isolation and sequencing of the 5' end of the rat microtubule-  
RT associated protein (MAP1B)-encoding cDNA.";  
RL Gene 172:307-308(1996).  
RN [2]  
RP SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION.  
RC STRAIN-Sprague-Dawley; TISSUE-Brain, and Gliat tumor;  
RX MEDLINE=92347374; PubMed=1639092;  
RA Zauner W., Kratz J., Staunton J., Feick P., Wiche G.;  
RT "Identification of two distinct microtubule binding domains on  
RT recombinant rat MAP 1B.";  
RL Eur. J. Cell Biol. 57:66-74(1992).  
RN [3]  
RP SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY.  
RC TISSUE-Spinal cord;  
RX MEDLINE=90059871; PubMed=2555150;  
RA Rientz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,  
RA Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.;  
RT "Neuraxin, a novel putative structural protein of the rat central  
RT nervous system that is immunologically related to microtubule-  
RT associated protein 5.";  
RL EMBO J. 8:2879-2888(1989).  
RN [4]  
RP DEVELOPMENTAL STAGE, AND PHOSPHORYLATION.  
RX MEDLINE=97405699; PubMed=9260743;  
RA Ma D., Nothias F., Boyne L.J., Fischer I.;  
RT "Differential regulation of microtubule-associated protein 1B (MAP1B)  
RT in rat CNS and PNS during development.";  
RL J. Neurosci. Res. 49:319-332(1997).  
CC -!- FUNCTION: The function of brain MAPS is essentially unknown.  
CC Phosphorylated MAP1B may play a role in the cytoskeletal changes  
CC that accompany neurite extension. Possibly MAP1B binds to at least  
CC two tubulin subunits in the polymer, and this bridging of subunits  
CC might be involved in nucleating microtubule polymerization and in  
CC stabilizing microtubules.  
CC -!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate  
CC with MAP1A and MAP1B proteins.

CC -!- TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem, cerebellum and cerebrum). Not expressed in liver, spleen, kidney, heart or muscle.

CC -!- DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic nerve levels are high early in development but decrease during postnatal development and are low in adults. In dorsal root ganglia levels remain high throughout development.

CC -!- INDUCTION: By nerve growth factor.

CC -!- DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAP1B to microtubules.

CC -!- PTM: LCI is coexpressed with MAP1B. It is a polypeptide generated from MAP1B by proteolytic processing. It is free to associate with both MAP1A and MAP1B. It interacts with the amino-terminal region of MAP1B (By similarity).

CC -!- PTM: Phosphorylated.

CC -!- SIMILARITY: TO MAP1A.

CC -!- CAUTION: A C-terminal fragment of this protein (residues 1597 to 2459) was originally described as neuraxin in Ref.3.

CC -----

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CC -----

DR EMBL; U52950; AAB17068.1; -

DR EMBL; X60370; CAC16162.1; -

DR EMBL; X16623; CAA34620.1; ALT\_SEQ.

DR PIR; A56577; A56577.

DR InterPro; IPR00102; MAP1B\_neuraxin.

DR Pfam; PF00414; MAP1B\_neuraxin; 10.

DR PROSITE; PS00230; MAP1B\_NEURAXIN; 8.

KW Microtubules; Repeat; Phosphorylation.

FT CHAIN ? 2459 MAP1 LIGHT CHAIN LCI.

FT REPEAT 1869 1885 MAP1B 1.

FT REPEAT 1886 1902 MAP1B 2.

FT REPEAT 1903 1919 MAP1B 3.

FT REPEAT 1920 1936 MAP1B 4.

FT REPEAT 1937 1953 MAP1B 5.

FT REPEAT 1954 1970 MAP1B 6.

FT REPEAT 1988 2004 MAP1B 7.

FT REPEAT 2005 2021 MAP1B 8.

FT REPEAT 2022 2038 MAP1B 9.

FT REPEAT 2039 2055 MAP1B 10.

FT DOMAIN 559 1035 GLU-RICH.

FT DOMAIN 588 786 LYS-RICH (HIGHLY BASIC, CONTAINS MANY KKEE AND KKEI/V REPEATS).

FT DOMAIN 2224 2312 LYS-RICH.

FT CONFLICT 127 127 M -> V (IN REF. 1).

FT CONFLICT 140 140 T -> S (IN REF. 1).

FT CONFLICT 2112 2112 R -> K (IN REF. 3).

FT CONFLICT 2169 2169 L -> I (IN REF. 3).

SQ SEQUENCE 2459 AA; 269497 MW; 2E3F6872DEDBBBA2 CRC64;

Query Match

Best Local Similarity 7.1%; Score 170.5; DB 1; Length 2459;

Matches 121; Conservative 73; Mismatches 196; Indels 145; Gaps 23;

QY 22 KPGSQDKSLHNRSLAERPLNQI-----AEAEKIKKTYPP---ENKPGQSNYSFVD 73

DB 549 KPLSSRSVKRESKEAPEATKASQVEKTPKVESKEKIVKDKPGKVESKP----- 599

QY 74 NLNLLRAITKEKIEROSIRSPDLNKLNVEDVSTNRKLLIDYDSTKSLDHFQD 133

DB 600 -----SVTEKVPSEKQSPVVAEVAEAKATESKPKVTOKDKVVKKEIKTKP---EBKKEE 651

QY 134 DP---DGLHQLDGTPLTAEDIVHIAAIIYEENDRAVFDKIVSKLLNLGLITESQAH--LE 190

DB 652 KPKKEVAKEDKTPLKDKDEKPKK-----EEAKKEIKKEEKKELKKEKVKETPLK 704

QY 191 DEVAEVLQKLSKEANNYEEDPNK-----PTSWTENOAG-----KIPEK 229

DB 705 DAKREV-KKEKKEKKEKEPKKEIKKIKKIDIKKSTPLSDTKKPAALKPKVAKKEPTK 763

QY 230 VTPMAA-IQD-GLAK-----GENDEIVSNLT-----TLTN 257

DB 764 KEPTAAGKLKDKGVKVIKKEGKTEAATAVGTAAVAAAAGVAASGPAKLEAERSLMS 823

QY 258 GLERRTKYSNDNFRDFOYFPNFVALLKSIDSEKAKE-----KETLIIMKTLI 307

DB 824 SPEDLTDFELKAEEDVAKDKPQLELEDEKLEKETEPEGEAYVYQKETEVS----- 877

QY 308 DFVKMMVKYGTISPEEGSVYLENDENIALQTNKL---EKNATDNISKL-----PPAP 358

DB 878 -----KGSAESPDGITTTEGE--CEQTPELEPVEKQGVDDIEKFEDEGAGFEES 928

QY 359 SEKSHEETDSTKEAAKMEKEYSGLKSDTNDNPGGKTDEPKKTEA--YLPAIRKNI 416

DB 929 SEAGDYEEKAFTAEAEPEEDG---EDNVSGSASKHSPTDEETAKAEADVHIKEKRESV 985

QY 417 -----EWLKHDKKGNKEDYDLKMRDFINKQADAYVEKGILKEEAE 459

DB 986 ASGDRAEDMDALEKGEAEQSEEGEEE-----DKAEDAREDEHPDKTEAE 1035

RESULT 9

BAG\_STRAG

ID BAG\_STRAG STANDARD; PRT; 1164 AA.

AC P27951;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE IGA FC receptor precursor (Beta antigen) (B antigen).

GN BAG.

OS Streptococcus agalactiae.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI\_TaxID=1311;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 38-48.

RC STRAIN-LA239;

RX MEDLINE=91312121; PubMed=1857207;

RA Jerlstroem P.G., Chhatwal G.S., Timmis K.N.;

RT "The Iga-binding beta antigen of the c protein complex of Group B streptococci: sequence determination of its gene and detection of two binding regions."

RT Mol. Microbiol. 5:843-849(1991).

RN [2]

RP IDENTIFICATION OF IG-LIKE DOMAIN.

RX MEDLINE=97035265; PubMed=8880921;

RA Bateman A., Eddy S.R., Chothia C.;

RT "Members of the immunoglobulin superfamily in bacteria.";

RL Protein Sci. 5:1939-1942(1996).

CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (potential).

CC -!- SIMILARITY: Contains 1 Immunoglobulin-like domain.

CC -----

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CC -----

DR EMBL; X59771; CAA2442.1; -

DR PIR; S15330; FCSOAG.

DR InterPro; IPR004829; Csurface\_antigen.

DR InterPro; IPR005877; Gpos\_YIRK..

DR InterPro; IPR001899; Gram\_pos\_anchor.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR006192; LPXIG.

DR Pfam; PF00746; Gram\_pos\_anchor; 1.

DR Pfam; PF05062; RICH; 1.  
DR Pfam; PF04650; YSRK.signal; 1.  
DR ProDom; PD153432; Csurface\_antigen; 1.  
DR SMART; SM00409; IG; 1.  
DR TIGRFAMS; TIGR01167; LPXG\_anchor; 1.  
DR TIGRFAMS; TIGR01168; YSRK.signal; 1.  
DR PROSITE; PS00847; GRAM\_POS\_ANCHORING; 1.  
DR PROSITE; PS00835; IG.LIKE; FALSE.NEG.  
KW Cell wall; Peptidoglycan-anchor; Receptor; Repeat; Signal;  
KW Immunoglobulin domain.  
FT SIGNAL 1 37  
FT CHAIN 38 1135 IGA FC RECEPTOR.  
FT PROPEP 1136 1164 REMOVED BY SORTASE (POTENTIAL).  
FT DOMAIN 434 534 IG-LIKE.  
FT DOMAIN 199 438 IGA-BINDING (POTENTIAL).  
FT DOMAIN 439 826 IGA-BINDING (POTENTIAL).  
FT DOMAIN 827 945 PRO-RICH REPEATS.  
FT SITE 1132 1136 LPXG SORTING SIGNAL (POTENTIAL).  
FT MOD\_RES 1135 1135 AMIDE-LINKED TO CELL WALL (POTENTIAL).  
SQ SEQUENCE 1164 AA; 131051 MW; 65DE94AF720A5474 CRC64;  
  
Query Match 7.1%; Score 169.5; DB 1; Length 1164;  
Best Local Similarity 21.4%; Pred. No. 0.41;  
Matches 123; Conservative 78; Mismatches 189; Indels 185; Gaps 25;  
  
QY 36 LSAERPLNE-----QIAAEEDKIKKTPPENKPGOSNFSVDNLLRAIT-EKEK 86  
DB 149 LELEQNFNTNRLHLHIKQHEVEKKAK-----QOKTLKQSDTKVDLSNIDELNHHQSQ 204  
QY 87 IEK--ERQSIRSPDNKL-----NVEDVDSYTKRKLIDYDSTKGLDHLK 130  
DB 205 VEKMAEQKITNEDKDSMLKKTIRKQAQADKKDAEVKREELGKLFSTKAGLDQE 264  
QY 131 FQDDPGLHQLDGTPLTAEDIVHKI-----AARIYENDRAVDKIVSKLLNLG 179  
DB 265 IQE-----HVKKET--SSEENTQKDEHYANSLQNLAAQSKLEELDKATTNEQATQVKNOF 317  
QY 180 L-----ITESAHTLEDEVAEV-----LQKLSKE---ANNYEE 210  
DB 318 LENAQKLKEIOLPIKETNVKLYKANSELEQVEKELKHNSLEANLEDLVAKSEIVREYEG 377  
QY 211 DPNKPSWTE-----NQAKIPEKVTYPMAAIODGLAKGENDTFSN 251  
DB 378 KLNQSKNLPLEKQLEBEAHSKLVQVVEDEFKFKFTSEQVTPKRVKRDIAANENNO---Q 434  
QY 252 TLTLNGLRRRTYSEDNFRQFPNFPYALLKSIDSEKAEKETLITIMKLILDFVK 311  
DB 435 KIETVSPENITVYEGED-----VKFTVTAKS-DS-----KTTLDLFS 471  
QY 312 MMVKG-TTSPGVSYLENLD-----EMIALQTK---NKLEKNATD 349  
DB 472 LTKYNPVSVDRISTNYKNTDNHKTAEITIKNLKNSQTVTLKAKDDSGNVVETFTI 531  
QY 350 NISKLPAPSEKSHETDSTKEAA-----KMEKEYGSLKD 385  
DB 532 TVQKKEEKQVPTPEQKDSKTEKVPQEPKSDKNQOLIKSAQAELEKLEKAIKELME 591  
QY 386 STKDDNSNGGKDEPKGTEYALEAIRNIEWLK-----HUKKGNKEDYDLSKMDFTN 441  
DB 592 Q-PEIPSNP--EYGIQKSWESQKEPIQEAITSFKKIIGDSSSKYTYEYFNKRYKSDFMN 648  
QY 442 QKADAVVEKGILDKAE-----AIKRIYSS 467  
DB 649 YQLHAQWE--MLTRKVQVMNKPDPNAEIKKIFES 681  
  
RESULT 10  
ID REST\_HUMAN STANDARD; PRT; 1427 AA.  
AC P30622;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Restin (Cytoplasmic linker protein-170 alpha-2) (CLIP-170) (Reed-  
Sternberg intermediate filament associated protein).  
GN RSN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Peripheral blood monocytes;  
RX MEDLINE=92289675; PubMed=1600942;  
RA Bilbe G., Delabie J., Brueggen J., Richener H., Asselbergs F.A.M.,  
RA Cerletti N., Sorg C., Odink K., Tarcsay L., Wiesendanger W.,  
RA de Wolf-peeters C., Shipman R.;  
RT "Restin: a novel intermediate filament-associated protein highly  
RT expressed in the Reed-Sternberg cells of Hodgkin's disease.";  
RL EMBO J. 11:2103-2113(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92405160; PubMed=1356075;  
RA Pierre P., Scheel J., Rickard J.E., Kreis T.E.;  
RT "CLIP-170 links endocytic vesicles to microtubules.";  
RL Cell 70:887-900(1992).  
CC -!- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASSOCIATED PROTEIN  
CC THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES.  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE  
CC CYTOSKELETON.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms-2;  
CC Name-Long;  
CC IsoId=P30622-1; Sequence-Displayed;  
CC Name-Short;  
CC IsoId=P30622-2; Sequence-VSP\_000765;  
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG CELLS  
CC OF HODGKIN'S DISEASE.  
CC -!- SIMILARITY: Contains 2 CAP-Gly domains.  
CC -----  
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CC -----  
CC EMBL; X64838; CA646050.1; -;  
DR EMBL; M97501; AAA35693.1; -;  
DR PIR; S22695; S22695.  
DR Genew; HGNC:10461; RSN.  
DR MIM; 179838; -;  
DR GO; GO:0005768; C:endosome; TAS.  
DR GO; GO:0005882; C:intermediate filament; TAS.  
DR GO; GO:0015630; C:microtubule cytoskeleton; TAS.  
DR GO; GO:0008017; F:microtubule binding activity; TAS.  
DR GO; GO:0006899; P:non-selective vesicle transport; TAS.  
DR InterPro; IPR000938; CAP-Gly.  
DR InterPro; IPR001878; Znf\_CCHC.  
DR Pfam; PF01302; CAP\_GLY; 2.  
DR SMART; SM00343; Znf\_C2HC; 1.  
DR PROSITE; PS00845; CAP\_GLY\_1; 2.  
DR PROSITE; PS0245; CAP\_GLY\_2; 2.  
DR Cytoskeleton; Microtubules; Coiled coil; Repeat; Alternative splicing.  
KW DOMAIN 78 120 CAP-GLY 1.  
FT DOMAIN 143 204 SER-RICH.  
FT DOMAIN 232 274 CAP-GLY 2.  
FT DOMAIN 304 331 SER-RICH.  
FT DOMAIN 350 1342 COILED COIL (POTENTIAL).  
FT DOMAIN 1408 1421 CCHC-BOX.  
FT VARSPIC 457 491 Missing (in isoform Short).  
FT /FTID=VSP\_000765.  
FT CONFLICT 1069 1069 D -> E (IN REF. 2).  
FT SEQUENCE 1427 AA; 160989 MW; 0A4F166DD94254E8 CRC64;  
SQ

```
Query Match 7.1%; Score 169.5; DB 1; Length 1427;
Best Local Similarity 22.0%; Pred. No. 0.52;
Matches 109; Conservative 79; Mismatches 184; Indels 123; Gaps 20;

OY 34 RELSAE-----RPLNEQIAAEEDKIKKTYPPENKPGOSNYSFVDNL-----NLRA 80
DB 769 KASSEGSEKMKLQQQL-EAAEKQIKHLEKNAESSKASITRELOGRELKTNQEN 827
OY 81 ITE-----REKIEKERQ-----SIRSPDL-----NVEDVDSTKN 113
DB 828 LSEVSQVETLEKELQILKEFAEASEAVSORSQMTVKNLHQKEQFNLSLDLEKL 887
OY 114 RKLDDYSTSGLDHKQDDPDGLHQLDGTPLTAEDIVHKAARIYEENDRAVDFKTVS 173
DB 888 RENLAD-----WEAKFERKDEREQL-----IKAKEKLEND-----IA 920
OY 174 KLLNGLITESQAHTLEDEV-----AEVLQKLISKEANNYE-----EDNKPPTSWTEN 221
DB 921 EIMKSGNSQOLTKMNDLRLKERDVEELQKLUTKANENASFLOKSTEDMTVRAEOSQ 980
OY 222 QAGKIPEKVTMAAIDQGLAKGENDTVSNLTTLTNGLERRTKTYSEDNFRDFQVFPNFY 281
DB 981 EAAKHHEE-----EKKELEKILSD-----LEKKMET-SHNOQCELEK-----1015
OY 282 ALLKSIDSEKAKETLITITWKTLIDPVKMMVKYGTISPEEGVSYLENLDEMIALQTKN 341
DB 1016 ARYERATSETTKHEEILQNLQKLTILDTEDLKG-----ARENSGLLQLEELRQKQADKA 1071
OY 342 KLEKNATDNISKLPAPSEKSH--EETDSTKEEAKEKYEKSLKDKSTKDNPNPGKTD 399
DB 1072 KAAQTAEDAMQIMQMTKEKTELTASLDTKTQNAKLQNLQELDTLKENNL-KNVEELNKS 1130
OY 400 EPKGTAYLEAIRKNIEWLKHH-----DKGNKEDYDLSKMRDFINKQADAYV 448
DB 1131 ELLTVENQKMEERKEIETLQAAAKSQOALSALQEEVKNLAELGLSRDVTSHQKLEE 1190
OY 449 EKGILDEEBAIRK 463
DB 1191 ERSVLNNQLEMKKR 1205

RESULT 11
RA50_METJA STANDARD; PRT; 1005 AA.
AC Q58718;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA double-strand break repair rad50 ATPase.
GN RAD50 OR MJ1322.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Sulton C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii".
RL Science 273:1058-1073(1996).
CC -!- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
CC rad50/mre11 complex possesses single-strand endonuclease activity
CC and ATP-dependent double-strand-specific exonuclease activity.
CC Rad50 provides an ATP-dependent control of mre11 by unwinding
```

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RBP2_PLAVB STANDARD; PRT; 1251 AA.
ID RBP2_PLAVB STANDARD; PRT; 1251 AA.
AC Q00799;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Reticulocyte binding protein 2 (Fragment).
GN RBP2.
OS Plasmodium vivax (strain Belém).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=31273;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92315338; PubMed=1617731;
RA Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;
RT "A reticulocyte-binding protein complex of Plasmodium vivax
merozoites";
RL Cell 69:1213-1226(1992).
CC -!- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO
CC HUMAN RETICULOCYTE CELLS.
CC -!- SUBCELLULAR LOCATION: Membrane-bound (Probable).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC EMBL; M88098; AAA29744.1; -.
DR Malaria; Receptor; Membrane.
KW NON_TER 1 1251
FT NON_TER 1251 1251
SQ SEQUENCE 1251 AA; 143741 MW; 54BA51C7404AC572 CRC64;

Query Match 7.0%; Score 168; DB 1; Length 1251;
Best Local Similarity 20.3%; Pred. No. 0.52;
Matches 100; Conservative 95; Mismatches 178; Indels 120; Gaps 23;

QY 27 QDKSLNRELASR---PLNEQIAEAEEDKIKTYPPENKPGQSNYS--FVD-NLNLRA 80.
DB 8 KDTSPDEKKKSIEKAYKMGNTLKELEKMDDEKIEVEEAQIQYKRFIDHVNLMND 67
QY 81 ITEKIEKEROSIRSPD---NKLNVEDVDSTKNRKLIDYDS-----122
DB 68 EVEKSLVMEKELYKEDEIKQKNEYKQDTSNFYTYEQYNSATQSKAKIEQFINIA 127
QY 123 -TKSGLDHFKPD-----DPDGLHQLDGTPLTAEDIV-----HKTA 156
DB 128 TTKKGTSDTSQDINELESIEKEVHKVLQVLKQESNMEEMKQILSMKDLILNNSETIA 187
QY 157 ARI-----YEENDRAVDFKIVSKLIN--LGLITESQAH-----TLED-----EVA 194
DB 188 KEISNNTQNALGFRENAKTKLKN--TDQLLRQAAMIEEAHAKHNNDIALEDAQIDTEVS 246
QY 195 EVLOKLIKEANNYEDBNKPTSWENQAGKIPEKVTPTMAAIODGLAKE---NDETVS 250
DB 247 KIEQ--INREIMNKKDEIKSYLSEIKYKDKCTTEISNKRKDKTEFLKPKPNESNS 304
QY 251 NTLITLNGLERRTKTYSEDNFRDQVFPNFIALLKSI-DSEKAEKKEKTLITIMKTLIDF 309
DB 305 NKNVINE-----INENIRNSEQY-----LKDIEDAEKQASTK-----336
QY 310 VKMWKYGITSPEGVSYLENDEMIALQTKNKLKNATNISKLPAPSEKSHETDST 369
DB 337 VELFHKH-----ETTISNFKSEILGVETKSKKINKAEDIMKETERHNSQTQVKGF 391
QY 370 KEAAKMEKEYGLKSDTDDNSNPGCKTDEPKGKTEAYLEAIRKNIEWLKHDKKGNKE 429
DB 392 QENLKNLNEPHN--YDNAEDELNN--DKSTNAKVLJETNLESYKHNLSI-TNIKOGGEK 446
QY 430 DVDLSKMRDFINK 442

447 IV--SKAKDIMQK 457
DB 447 IV--SKAKDIMQK 457

RESULT 13
TRDN_CANFA STANDARD; PRT; 700 AA.
ID TRDN_CANFA STANDARD; PRT; 700 AA.
AC P82179;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Triadin.
GN TRDN.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX TISSUE=Heart, and Skeletal muscle;
RX MEDLINE=99428545; PubMed=10497235;
RA Kobayashi Y.M., Jones L.R.;
RT "Identification of triadin 1 as the predominant triadin isoform
expressed in mammalian myocardium.";
RL J. Biol. Chem. 274:28660-28668(1999).
CC -!- FUNCTION: MAY BE INVOLVED IN ANCHORING CALSEQUESTRIN TO THE
CC JUNCTIONAL SARCOPLASMIC RETICULUM AND ALLOWING ITS FUNCTIONAL
CC COUPLING WITH THE RYANODINE RECEPTOR (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Sarcoplasmic
CC reticulum.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Skeletal;
CC IsoId=P82179-1; Sequence=Displayed;
CC Name=Cardiac 1; Sequence=VSP_004001, VSP_004002;
CC IsoId=P82179-2; Sequence=VSP_004003, VSP_004004;
CC Name=Cardiac 3;
CC IsoId=P82179-3; Sequence=VSP_004005;
CC -!- TISSUE SPECIFICITY: SKELETAL AND CARDIAC MUSCLE.
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CC EMBL; AF165916; AAF00222.1; -.
DR EMBL; AF165915; AAF00221.1; -.
DR EMBL; AF165917; AAF00223.1; -.
KW Transmembrane; Sarcoplasmic reticulum; Glycoprotein;
KW Alternative splicing.
FT INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 47 67 POTENTIAL.
FT DOMAIN 68 700 LUMENAL (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC... ) (POTENTIAL).
FT VARSPLIC 257 277 DQYAFCRYMIDMFVHGDRLPG -> GKHSSEVAGSGSKRTLGL
FT FT KQIQ (in isoform Cardiac 1).
FT FT /FTId=VSP_004001.
FT FT Missing (in isoform Cardiac 1).
FT FT /FTId=VSP_004002.
FT FT E -> EPIKKEVKVPGSLKEKE (in isoform
FT FT Cardiac 3).
FT FT /FTId=VSP_004003.
FT FT EEKVKQVATEKAALAEKTVKPKAKAHOEKESPTIKTD
FT FT KPKPTSKETPEVTES -> GILQVVPVNLCLFLVQFQODE
FT FT ELNVESKVFPMHVLVSHPTSRTSPILVISTCIRT (in
FT FT isoform Cardiac 3).
FT FT /FTId=VSP_004004.
FT FT SEQUENCE 700 AA; 78152 MW; F033E3AA1BEE0C56 CRC64;
SQ
```

```
Query Match      6.9%; Score 166; DB 1; Length 700;
Best Local Similarity 20.2%; Pred. No. 0.32;
Matches 98; Conservative 75; Mismatches 175; Indels 136; Gaps 19;

QY 27 QDKSLH-----NRELSAERPLNEQTAEAEDKIKKTYPPENKPGOSNYSFVDNLLNLLRAIT 82
DB 139 KQELHKEAEEKPERKILAKVAHREKKEKSEK-----AT 181
QY 83 EKEKEKERSIRSPDLNKLNVEDVSTKRNKLLDDYDSTKSLDGHKFDODDGLHOLD 142
DB 182 HKXIEKKEP-----ETKMAEERKAKTEKIK--KEVKGQEKVKYTAAKVQ 233
QY 143 GTPATAEDIVHKIARI--YEENDRAVPDKIVSKLLNGLLITESQAHTL----- 189
DB 234 KTPPKAKEGKETAATAAKHEQKQYAFRCYRMYDMFVHGDLRPGQSPALPPLPTVQASR 293
QY 190 -----EDEVAEVLQKLSKEANNYEEDNPKPTS-----WTENOAGKIPE--- 228
DB 294 PTPASPTLEGKEEKKKAERKVTSETKKKEKEDVKKSKDKDTAIDVEKKEPGKAPETKQ 353
QY 229 ---KVTMAAQQDLAKGENDETVNTLTITNGLERTKTYSEDNFRDQFVPFNYALLK 285
DB 354 GTIKVQAQAAK-----KDEKED-----SKTKTPVEH----- 383
QY 286 SIDSEKAKEKETITIMKTLLIDFVMMVMVYGTISPEEGVSYLENDEMIALQTKNKLEK 345
DB 384 --PRGKKQEKKEKVEPAKS-----SKHEKAPSE-----KQVKAKTERAKEE 424
QY 346 NATDNISKLPAPSEKSHEDSTKEEAKEKVEKSLKDKSTKDDNSNPGKTDK--PKG 403
DB 425 TSAASTKAVPG---KKEKTKTVEQIRKEK---SGKTSTASKDKEPEIKDKMPKA 478
QY 404 KTEAYLAIRKNIEMLKHD---KKGKEDYDLKMRDFIN-----KQADAYVEKG 451
DB 479 DKEVKRPQSQVKKEKSEKQVKEAKPEQDIAPKPTVSHGKPEEKVKQVKA--TEKA 537
QY 452 ILDK 455
DB 538 AIEK 541

RESULT 14
KF5C_HUMAN
ID KF5C_HUMAN STANDARD; PRT; 957 AA.
AC O60282; G95079;
DT 16-OCT-2001 (Rel. 40, Created)
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RC TISSUP-Brain;
RX MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:31-39(1998).
RP [2]
RP SEQUENCE OF 355-585 FROM N.A.
RA Engelender S., Sharp A.H., Colomer V., Tokito M.K., Lanahan A.,
RA Worley P., Holzbaur E.L.F., Ross C.A.;
RT "Huntingtin associated protein 1 (HAP1) interacts with the p150Glued
RT subunit of dynactin.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
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RX MEDLINE-93024922; PubMed-1406971;
RA Yen T.J., Li G., Schaar B.T., Szilak I., Cleveland D.W.;
RT "CENP-E is a putative kinetochore motor that accumulates just before
RT mitosis.";
RL Nature 359:536-539(1992).
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RX MEDLINE-95196755; PubMed-7889940;
RA Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;
RT "Mitotic HeLa cells contain a CENP-E-associated minus end-directed
RT microtubule motor.";
RL EMBO J. 14:918-926(1995).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE-98437347; PubMed-9763420;
RA Chan G.K.T., Schaar B.T., Yen T.J.;
RT "Characterization of the kinetochore binding domain of CENP-E reveals
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RL J. Cell Biol. 143:49-63(1998).
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CC AND/OR SPINDLE ELONGATION.
CC -!- SUBUNIT: INTERACTS WITH CENP-F AND BUBR1 KINASE.
CC -!- SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CC CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AND IS
CC QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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AUTHORS Eaton,D.L., Filvaroff,B., Gerritsen,M.E., Goddard,A.,  
Gadowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and  
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LOCUS  
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ACCESSION AX463956  
VERSION AX463956.1 GI:21898995  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,  
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,  
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,  
Wood,W.L. and Zhang,Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
same  
JOURNAL Patent: WO 0140466-A 89 07-JUN-2001;  
Genentech Inc. (US)  
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Best Local Similarity 99.7%; Pred. No. 0;

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RESULT 4
BD127901
LOCUS
DEFINITION
ACCESSION BD127901
VERSION
KEYWORDS JP 2002017375-A/3332
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 1871)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
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Primer for synthesizing full-length cDNA and use thereof  
Patent: JP 2002017375-A 3332 22-JAN-2002;  
HELIX RESEARCH INSTITUTE  
OS Homo sapiens (human)  
PN JP 2002017375-A/3332  
PD 22-JAN-2002  
PF 07-JUL-2000 JP 2000253172  
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO  
ISHII,  
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SHINICHI KOJIMA,  
PI TETSUJI OTSUKI,HISASHI KOGA  
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Primer for synthesizing full-length cDNA and use thereof FH Key

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BASE COUNT 677 a 389 c 385 g 420 t  
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Query Match 92.3%; Score 1861.4; DB 6; Length 1871;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1865; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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ACCESSION AK075314
VERSION AK075314.1 GI:22761322
KEYWORDS oligo capping; fis (full insert sequence).
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ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS Isoqai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saiko,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and Ninomiya,K.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1871)
AUTHORS Isoqai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2002) Takao Isoqai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).
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Best Local Similarity 99.7%; Pred. No. 0;
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Qy 24 CTCGCCGTACAGGAACTTCAGACCCACAGGGCGGACAGCGCTCCCTCTACCTGGAGA 83
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http://www.systemsbio.org  
contact: amadan@systemsbio.org  
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia  
Greene, Mark Kettman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
Series: IRAL Plate: 19 Row: 1 Column: 10  
This clone was selected for full length sequencing because it  
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Location/Qualifiers

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AX305318
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DEFINITION Sequence 69 from Patent WO0188188.
ACCESSION AX305318
VERSION AX305318.1 GI:17644886
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
AUTHORS Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.
TITLE Method for examining ischemic conditions
JOURNAL Patent: WO 0188188-A 69 22-NOV-2001;
School Juridical Person Nihon University (JP)
FEATURES
Location/Qualifiers
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BASE COUNT 708 a 522 c 496 g 437 t
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Query Match 61.2%; Score 1235.4; DB 6; Length 2163;
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Matches 1596; Conservative 0; Mismatches 357; Indels 37; Gaps 11;
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MMSGIII

LOCUS MMSGIII 2163 bp mRNA linear ROD 07-DEC-1994

DEFINITION Mus musculus secretogranin III (SgIII) mRNA, complete cds.

ACCESSION U02982

VERSION U02982.1 GI:413763

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 2163)

AUTHORS Dopazo, A., Lovenberg, T.W., Danielson, P.E., Ottiger, H.P. and Sutcliffe, J.G.

TITLE Primary structure of mouse secretogranin III and its absence from deficient mice

JOURNAL J. Mol. Neurosci. 4 (4), 225-233 (1993)

MEDLINE 95001263

PUBMED 7917832

REFERENCE 2 (bases 1 to 2163)

AUTHORS Dopazo, A.

TITLE Direct Submission

JOURNAL Submitted (28-OCT-1993) Dopazo A., The Scripps Research Institute, Molecular Biology, 10666 N. Torrey Pines Rd., La Jolla, CA 92037, USA

FEATURES

source Location/Qualifiers

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BASE COUNT 708 a 522 c 496 g 437 t

ORIGIN

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Best Local Similarity 80.2%; Pred. No. 2.5e-253;

Matches 1596; Conservative 0; Mismatches 357; Indels 37; Gaps 11;

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Mus musculus secretogranin III, mRNA (cdna clone MGC:36181  
IMAGE:5362975), complete cds.  
ACCESSION BC024785  
VERSION BC024785.1 GI:19353444  
KEYWORDS MGC.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 2175)  
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klusner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, J.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Maman, A., Rodrigues, S., Sanchez, A., Whitting, M., Maman, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smal, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

**TITLE** Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
**MEDLINE** 22388257  
**PUBMED** 12477932  
**REFERENCE** 2 (bases 1 to 2175)  
**AUTHORS** Strausberg, R.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
**REMARK** NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
**COMMENT** Contact: MGC help desk  
 Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)  
 Tissue Procurement: The Cepko Laboratory  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 53 Row: d Column: 22  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6677866.

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BASE COUNT 730 a 520 c 490 g 435 t  
 ORIGIN

Query Match 59.1%; Score 1192.2; DB 10; Length 2175;  
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1960	Qy	CTTTGGGAAA 1969	
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RESULT 11			
BC009511			
LOCUS		941 bp mRNA linear PRI 12-JUL-2001	
DEFINITION		Homo sapiens, clone IMAGE:3537207, mRNA, partial cds.	
ACCESSION		BC009511	
VERSION		BC009511.1 GI:14550521	
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SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
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		Strausberg,R.	

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Qy 1771 AAAATTTTTCACCAAGGGTTATTAGAAAGTCTGAATTTACAGTAGTATTAACTTTAC 1830

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Qy 1891 GCTGAGA 1897

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RESULT 12

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LOCUS BD125387 799 bp DNA linear PAT 18-SEP-2002

DEFINITION Primer for synthesizing full-length cDNA and use thereof.

ACCESSION BD125387

VERSION BD125387.1 GI:23220332

KEYWORDS JP 2002017375-A/818.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H.

TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002017375-A 818 22-JAN-2002;

COMMENT HELIX RESEARCH INSTITUTE

OS Homo sapiens (human)

PN JP 2002017375-A/818

PD 22-JAN-2002

PF 07-JUL-2000 JP 2000253172

PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO

PI ISHII,

PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI

SHINICHI KOJIMA,

PI TETSUJI OTSUKI,HISASHI KOGA

PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC

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PC C12P21/02,C12Q1/68/C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC

Primer for synthesizing full-length cDNA and use thereof FH key

Location/Qualifiers

FT source i. .799

FEATURES

source

FT Location/Qualifiers

1. .799

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BASE COUNT 242 a 206 c 168 g 180 t 3 others

ORIGIN

Query Match 37.6%; Score 757.8; DB 6; Length 799;

Best Local Similarity 97.4%; Pred. No. 2.8e-151;

Matches 779; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

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Db 1 CTCGCGCTCAGAGAACTTTCAGCACCCACAGGGGGGAGCAGCGCTCCCTCTACCTGGAGA 60

Qy 84 CTTGACTCCCGCGCGGCCCAACCCCTGTATTCCTTTCAGCTGAGTGTGAGATCCTG 143

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Qy 144 CAGCGGCCAGTCCGCGGCCCTCTCCGCCCCCACCCACCTCTCTGCTCTCTCTGCTTT 203

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Qy 324 AGTGCTCCGATTCAAGCTTTCCCAACCTTGGAGGAGCCAGACAATCTCTACATAA 383

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Db 481 TAAGTTGAACCTGCTAAGGCAATAACAGAAAAAGAAAAATTGAGAAAGAAAGACAATC 540

Qy 564 TATAAGAGCTCCCACTTTGATAAAGTTGAATGTGAAGATGTTGATTCAACCAAGAA 623

Db 541 TATAAGAGCTCCCACTTTGATAAAGTTGAATGTGAAGATGTTGATTCAACCAAGAA 600

Qy 624 TCGAAACTGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 683

Db 601 TCGAAACTGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660

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Db 661 TGATCCAGATGCTCTTCATCAACTAGACGGGACCTCTTAACCGCTGAAGACATTTGCCA 719

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Qy 804 TAAACTACTTAACTCTCGGCC 823

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RESULT 13

BD126925

LOCUS BD126925 799 bp DNA linear PAT 18-SEP-2002



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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 799)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Primer for synthesizing full-length cDNA and use thereof
PATENT: JP 2002017375-A 2356 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2356
PD 22-JAN-2002
PF 07-JUL-2000 JP 200253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
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PD 15-JAN-2002
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PR 05-AUG-1999 US 60/147499
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REFERENCE
AUTHORS    Holthuis, J.C. and Martens, G.J.
TITLE      The neuroendocrine proteins secretogranin II and III are regionally
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            Xenopus intermediate pituitary
JOURNAL    J. Neurochem. 66 (6), 2248-2256 (1996)
MEDLINE    96217355
PUBMED     8632145
REFERENCE  2 (bases 1 to 2036)
AUTHORS    Holthuis, J.C.M.
TITLE      Direct Submission
JOURNAL    Submitted (07-NOV-1995) J.C.M. Holthuis, KUN, Dept. Animal
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 Rattus.  
 REFERENCE 1 (bases 1 to 2146)  
 AUTHORS Dopazo A., Lovenberg, T.W., Danielson, P.E., Ottiger, H.P. and  
 Sutcliffe, J.G.  
 TITLE Primary structure of mouse secretogranin III and its absence from  
 deficient mice  
 J. Mol. Neurosci. 4 (4), 225-233 (1993)  
 JOURNAL 95001263  
 MEDLINE 7917832  
 PUBMED  
 REFERENCE 2 (bases 1 to 2146)  
 AUTHORS Dopazo, A.  
 TITLE Direct Submission  
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 Molecular Biology, 10566 N. Torrey Pines Rd., La Jolla, CA 92037,  
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